

Query Match	99.2%;	Score 422.4;	DB 4;	Length 444;
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QY	181	ATCTTCCAGGAGTACCCTGTATGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGT	240	
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QY	241	ATGCGATCGGGGGCTGCTGCAATGACGAGGCCCTGGAGTGTGTGCCACTGAGGAGTCC	300
Ddb	241	ATGCGATCGGGGGCTGCTGCAATGACGAGGCCCTGGAGTGTGTGCCACTGAGGAGTCC	300
QY	301	RACATCACCATTGCAGATTATGCGGATCAAACCTCACCAAGCCCAGCACATAGGAGAGTG	360
Ddb	301	RACATCACCATTGCAGATTATGCGGATCAAACCTCACCAAGCCCAGCACATAGGAGAGTG	360
QY	361	AGCTTCCTACAGCAACAATAATGTAATGCAGACAAAGAAGATAGAGCAAGACAAGAA	420
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Ddb	421	AAAT 424	
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; Sequence 1, Application US/08718904			
; Patent No. 6037329			
; GENERAL INFORMATION:			
; APPLICANT: Baird, J. Andrew			
; APPLICANT: Chandler, Lois Ann			
; APPLICANT: Sosnowski, Barbara A.			
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS			
; NUMBER OF SEQUENCES: 128			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SEED and BERRY LLP			
; STREET: 6300 Columbia Center, 701 Fifth Avenue			
; CITY: Seattle			
; STATE: Washington			
; COUNTRY: USA			
; ZIP: 98104-7092			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/718,904			
; FILING DATE: 24-SEP-1996			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: No. 6037329tenburg Ph.D., Carol			
; REGISTRATION NUMBER: 39,317			
; REFERENCE/DOCKET NUMBER: 760100.415C1			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (206) 622-4900			
; TELEFAX: (206) 682-6031			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 473 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: both			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 13..456			
; OTHER INFORMATION: /product= "VEGF121-encoding DNA"			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 13..90			
; OTHER INFORMATION: /product= leader-encoding sequence			
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Db 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLOHKKCECRPKDRARQEK 141  
Db 121 SFLOHKKCECRPKDRARQEK 141

RESULT 2  
US-09-392-932-1  
; Sequence 1, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-392-932-1

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Best Local Similarity 100.0%; Pred. No. 2.7e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
Db 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLOHKKCECRPKDRARQEK 141  
Db 121 SFLOHKKCECRPKDRARQEK 141

RESULT 3  
US-08-706-054A-4  
; Sequence 4, Application US/08706054A  
; Patent No. 6451764  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: VEGF-Related Protein  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,054A  
; FILING DATE: 30-Aug-1996  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/003491  
; FILING DATE: 08-Sep-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: P-40,378  
; REFERENCE/DOCKET NUMBER: P0963R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 147 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-706-054A-4

Query Match 100.0%; Score 792; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 2.7e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
Db 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLOHKKCECRPKDRARQEK 141  
Db 121 SFLOHKKCECRPKDRARQEK 141

RESULT 4  
5240848-11  
; Patent No. 5240848  
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR  
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/337,037  
; FILING DATE: 10-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 274,061  
; FILING DATE: 21-NOV-1988  
; SEQ ID NO: 11:  
; LENGTH: 214  
5240848-11

Query Match 100.0%; Score 792; DB 6; Length 214;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
Db 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLOHKKCECRPKDRARQEK 141  
Db 121 SFLOHKKCECRPKDRARQEK 141

RESULT 5  
US-08-807-992B-3  
; Sequence 3, Application US/08807992B





GenCore version 5.1.3  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

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- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*
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- 5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	792	100.0	516	3	US-08-784-551C-1
5	792	100.0	642	4	US-09-392-932-9
6	792	100.0	648	3	US-08-586-039B-48
7	792	100.0	677	3	US-08-718-904-3
8	792	100.0	677	5	PCT-US95-10973A-27
9	792	100.0	699	4	US-09-392-932-10
10	792	100.0	728	3	US-08-718-904-4
11	792	100.0	728	5	PCT-US95-10973A-28
12	792	100.0	774	3	US-08-765-340-1

13	792	100.0	1195	6	5240848-6	Patent No. 5240848
14	792	100.0	1212	5	PCT-US95-10973A-31	Sequence 31, Appl
15	787	99.4	576	4	US-09-392-932-8	Sequence 8, Appl
16	787	99.4	605	3	US-08-718-904-2	Sequence 2, Appl
17	787	99.4	605	5	PCT-US95-10973A-26	Sequence 26, Appl
18	787	99.4	989	6	5332671-11	Patent No. 5332671
19	787	99.4	990	3	US-08-567-200A-1	Sequence 1, Appl
20	787	99.4	990	3	US-08-691-794-1	Sequence 1, Appl
21	787	99.4	990	4	US-08-882-816-1	Sequence 1, Appl
22	787	99.4	1369	5	PCT-US95-10973A-33	Sequence 33, Appl
23	783	98.9	516	4	US-09-392-932-7	Sequence 7, Appl
24	781.5	98.7	456	5	PCT-US95-10973A-88	Sequence 88, Appl
25	781.5	98.7	467	5	PCT-US95-10973A-86	Sequence 86, Appl
26	776.5	98.0	599	5	PCT-US95-10973A-87	Sequence 87, Appl
27	776.5	98.0	599	5	PCT-US95-10973A-89	Sequence 89, Appl
28	717.5	90.6	1543	6	5332671-5	Patent No. 5332671
29	685.5	86.6	445	3	US-08-586-039B-32	Sequence 32, Appl
30	685.5	86.6	649	3	US-08-586-039B-34	Sequence 34, Appl
31	680.5	85.9	573	3	US-08-586-039B-30	Sequence 30, Appl
32	657	83.0	886	6	5219739-23	Patent No. 5219739
33	656.5	82.9	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
34	656.5	82.9	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
35	651.5	82.3	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	649.5	82.0	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
37	640	80.8	498	6	5194596-20	Patent No. 5194596
38	640	80.8	498	6	5219739-21	Patent No. 5219739
39	640	80.8	1269	5	PCT-US95-10973A-32	Sequence 32, Appl
40	570.5	72.0	961	6	5219739-16	Patent No. 5219739
41	562.5	71.0	981	6	5194596-16	Patent No. 5194596
42	525	66.3	789	6	5219739-8	Patent No. 5219739
43	525	66.3	790	6	5194596-8	Patent No. 5194596
44	366	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	325	41.0	450	3	US-08-586-039B-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

Sequence 6' Application US/09392932-6  
US-09-392-932-6

Patent No. 6352975  
GENERAL INFORMATION:  
APPLICANT: Schreiner, George F.  
TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
FILE REFERENCE: SCIOS.002A  
CURRENT APPLICATION NUMBER: US/09/392,932  
CURRENT FILING DATE: 1999-09-09  
EARLIER APPLICATION NUMBER: 60/099,694  
EARLIER FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 444  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-392-932-6

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Length: 444  
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Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 100.00%  
Indels: 0  
DB: 4  
Gaps: 0

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 20, 2002, 03:26:39 ; Search time 58 Seconds

(without alignments)  
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Title: US-09-884-050-1

Perfect score: 426

Sequence: 1 atgaacttctgtctgtctg.....gagcaagacaagaagtaa 426

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	422.8	99.2	516	US-08-784-551C-1	Sequence 1, Appli
2	422.8	99.2	648	US-08-586-039B-48	Sequence 48, Appl
3	422.8	99.2	1195	5240848-6	Patent No. 5240848
4	422.4	99.2	444	US-09-392-932-6	Sequence 6, Appli
5	422.4	99.2	473	US-08-718-904-1	Sequence 1, Appli
6	422.4	99.2	473	PCT-US95-10973A-25	Sequence 25, Appl
7	422.4	99.2	774	US-08-765-340-1	Sequence 1, Appli
8	422	99.1	605	US-08-718-904-2	Sequence 2, Appli
9	422	98.1	605	PCT-US95-10973A-26	Sequence 26, Appl
10	421.2	98.9	516	US-09-392-932-7	Sequence 7, Appli
11	421.2	98.9	642	US-09-392-932-9	Sequence 9, Appli
12	421.2	98.9	677	US-08-718-904-3	Sequence 3, Appli
13	421.2	98.9	677	PCT-US95-10973A-27	Sequence 27, Appl
14	421.2	98.9	699	US-09-392-932-10	Sequence 10, Appl
15	421.2	98.9	728	US-08-718-904-4	Sequence 4, Appli
16	421.2	98.9	728	PCT-US95-10973A-28	Sequence 28, Appl
17	420.8	98.8	1212	US-08-586-039B-31	Sequence 31, Appl
18	420.4	98.7	576	US-09-392-932-8	Sequence 8, Appli
19	420.4	98.7	989	5332671-11	Patent No. 5332671
20	420.4	98.7	990	US-08-567-200A-1	Sequence 1, Appli
21	420.4	98.7	990	US-08-691-794-1	Sequence 1, Appli
22	420.4	98.7	990	US-08-882-816-1	Sequence 1, Appli
23	420.4	98.7	1369	PCT-US95-10973A-33	Sequence 33, Appl
24	409.4	96.1	456	PCT-US95-10973A-88	Sequence 88, Appl
25	409.4	96.1	467	PCT-US95-10973A-86	Sequence 86, Appl
26	409	96.0	599	PCT-US95-10973A-87	Sequence 87, Appl
27	409	96.0	599	PCT-US95-10973A-89	Sequence 89, Appl

28	366	85.9	1543	6	5332671-5	Patent No. 5332671
29	344.4	80.8	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
30	344	80.8	498	6	5194596-20	Patent No. 5194596
31	342.8	80.5	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
32	342.8	80.5	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
33	342.4	80.4	498	6	5219739-21	Patent No. 5219739
34	342.4	80.4	1269	5	PCT-US95-10973A-32	Sequence 32, Appl
35	342.4	80.4	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	325.2	76.3	649	3	US-08-586-039B-34	Sequence 34, Appl
37	324.8	76.2	445	3	US-08-586-039B-32	Sequence 32, Appl
38	324.4	76.2	573	3	US-08-586-039B-30	Sequence 30, Appl
39	293.6	68.9	961	6	5219739-16	Patent No. 5219739
40	290.4	68.2	961	6	5194596-16	Patent No. 5194596
41	271	63.6	789	6	5219739-8	Patent No. 5219739
42	271	63.6	790	6	5194596-8	Patent No. 5194596
43	250	58.7	886	6	5219739-23	Patent No. 5219739
44	197	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	134.4	31.5	146	3	US-08-765-340-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-08-784-551C-1  
; Sequence 1, Application US/08784551C  
; Patent No. 6013780  
; GENERAL INFORMATION:  
; APPLICANT: Gera Neufeld  
; APPLICANT: Eli Keshet  
; APPLICANT: Israel Vlodavsky  
; APPLICANT: Zoya Poltorak  
; TITLE OF INVENTION: ANGIOGENIC FACTOR AND USE THEREOF  
; TITLE OF INVENTION: IN TREATING CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blank, Rome, Comisky & McCauley LLP  
; STREET: 900 17th Street, N.W.  
; STREET: Suite 1000  
; CITY: Washington, D.C.  
; STATE: N/A  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,551C  
; FILING DATE: January 21, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Herbert  
; REGISTRATION NUMBER: 25,109  
; REFERENCE/DOCKET NUMBER: 0274.005/P003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 463-7700  
; TELEFAX: (202) 463-6915  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 516 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-784-551C-1

Query Match 99.2% Score 422.8; DB 3; Length 516;



Db 157 ATGAACCTTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTTGCTGCTCTACCTCCACCAT 216  
Qy 61 GCCAAGTGTGTCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGCAATCATCACCAAGTG 120  
Db 217 GCCAAGTGTGTCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGCAATCATCACCAAGTG 276  
Qy 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCCCTGTGTGAC 180  
Db 277 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCCCTGTGTGAC 336  
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 337 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 396  
Qy 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATCC 300  
Db 397 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATCC 456  
Qy 301 AACATCAGCATGCAGATGATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 360  
Db 457 AACATCAGCATGCAGATGATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 516  
Qy 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGCCAAAGAAAGATAGAGCAAGAA 420  
Db 517 AGCTTCTTACAGCAACAATAATGTGAATGCCAGCCAAAGAAAGATAGAGCAAGAA 576  
Qy 421 AAGTAA 426  
Db 577 AAAAAA 582

RESULT 4  
US-09-392-932-6  
; Sequence 6, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392.932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-6

Query Match 99.2%; Score 422.4; DB 4; Length 444;  
Best Local Similarity 99.8%; Pred. No. 7.5e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAACCTTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTTGCTGCTCTACCTCCACCAT 60  
Db 1 ATGAACCTTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTTGCTGCTCTACCTCCACCAT 60  
Qy 61 GCCAAGTGTGTCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGCAATCATCACCAAGTG 120  
Db 61 GCCAAGTGTGTCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGCAATCATCACCAAGTG 120  
Qy 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCCCTGTGTGAC 180  
Db 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCCCTGTGTGAC 180  
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240

Qy 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATCC 300  
Db 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATCC 300  
Qy 301 AACATCAGCATGCAGATGATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 360  
Db 301 AACATCAGCATGCAGATGATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 360  
Qy 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGCCAAAGAAAGATAGAGCAAGAA 420  
Db 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGCCAAAGAAAGATAGAGCAAGAA 420  
Qy 421 AAGT 424  
Db 421 AAAT 424

RESULT 5  
US-08-718-904-1  
; Sequence 1, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..456  
; OTHER INFORMATION: /product= "VEGF121-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= leader-encoding sequence  
US-08-718-904-1

Query Match 99.2%; Score 422.4; DB 3; Length 473;  
Best Local Similarity 99.8%; Pred. No. 7.7e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGAACCTTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTTGCTGCTCTACCTCCACCAT 60  
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FILING DATE: 27-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 311130/94  
FILING DATE: 21-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SERUNIAN, LESLIE  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 1452-4005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 774 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
US-08-765-340-1

Query Match 99.2%; Score 422.4; DB 3; Length 774;  
Best Local Similarity 99.8%; Pred. No. 9.7e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATTTCTGCTGCTTTGGTGATGGAGCCCTTGCTGCTCTACCTCCACCAT 60  
Db 101 ATGAATTTCTGCTGCTTTGGTGATGGAGCCCTTGCTGCTCTACCTCCACCAT 160

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 120  
Db 161 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 220

Qy 121 GTGAAGTTTCATGGATGTTCTATCAGGCGCAGCTACTGCCATCCAAATCGAGACCTGTGTGGAC 180  
Db 221 GTGAAGTTTCATGGATGTTCTATCAGGCGCAGCTACTGCCATCCAAATCGAGACCTGTGTGGAC 280

Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 281 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 340

Qy 241 ATGGATCGGGGGCTGCTGCAATCAGGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 300  
Db 341 ATGGATCGGGGGCTGCTGCAATCAGGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 400

Qy 301 AACATCACCATCGAGATTATCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 360  
Db 401 AACATCACCATCGAGATTATCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 460

Qy 361 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 420  
Db 461 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 520

Qy 421 AAGT 424  
Db 521 AAAT 524

RESULT 8  
US-08-718-904-2  
Sequence No. 2, Application US/08718904  
Patent No. 6037329  
GENERAL INFORMATION:  
APPLICANT: Baird, J. Andrew  
APPLICANT: Chandler, Lois Ann  
APPLICANT: Sosnowski, Barbara A.  
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA

ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/718.904  
FILING DATE: 24-SEP-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6037329tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.415C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 605 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..588  
OTHER INFORMATION: /product= "VEGF165-encoding DNA"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..90  
OTHER INFORMATION: /product= "leader sequence-encoding DNA"  
US-08-718-904-2

Query Match 99.1%; Score 422; DB 3; Length 605;  
Best Local Similarity 100.0%; Pred. No. 1.1e-119;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTTCTGCTGCTTTGGTGATGGAGCCCTTGCTGCTCTACCTCCACCAT 60  
Db 13 ATGAATTTCTGCTGCTTTGGTGATGGAGCCCTTGCTGCTCTACCTCCACCAT 72

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 120  
Db 73 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 132

Qy 121 GTGAAGTTTCATGGATGTTCTATCAGGCGCAGCTACTGCCATCCAAATCGAGACCTGTGTGGAC 180  
Db 133 GTGAAGTTTCATGGATGTTCTATCAGGCGCAGCTACTGCCATCCAAATCGAGACCTGTGTGGAC 192

Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 193 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 252

Qy 241 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 300  
Db 253 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 312

Qy 301 AACATCACCATCGAGATTATCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 360  
Db 313 AACATCACCATCGAGATTATCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 372

Qy 361 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 420  
Db 373 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 432

Qy 421 AA 422  
Db 433 AA 434

RESULT 9  
PCT-US95-10973A-26

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QY 361 AGCTTCTCAGCACACAACAAATGTGAATGCAGAGCCAAAGAAAAGATAGACCAACAAGAA 432
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Db 373 AGCTTCTCAGCACACAACAAATGTGAATGCAGAGCCAAAGAAAAGATAGACCAACAAGAA 432
      |||
QY 421 AA 422
      ||
Db 433 AA 434

RESULT 10
US-09-392-932-7
; Sequence 7, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-392-932-7

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Db	121	GTGAAGTTTCATGATGCTATCAGCGCAGCTACTGCGATCCCAATCAGACCCCTGGTGGAC	180
Qy	181	ATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTG	240
Db	181	ATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTG	240
Qy	241	ATGCGATGCGGGGCTGCTGCAATGACGAGGGGCTGGAGTGTGTGCCCACTAGAGGAGTCC	300
Db	241	ATGCGATGCGGGGCTGCTGCAATGACGAGGGGCTGGAGTGTGTGCCCACTAGAGGAGTCC	300
Qy	301	AACATCACCATGCAGATTATGCGGATCAAACTTACCAGAGCCAGACACATAGCAGAGATG	360
Db	301	AACATCACCATGCAGATTATGCGGATCAAACTTACCAGAGCCAGACACATAGCAGAGATG	360
Qy	361	AGCTTCTTACAGCACACAATGTGAATGCAGACCAAGAAAGATAGACCAACACAAGAA	420
Db	361	AGCTTCTTACAGCACACAATGTGAATGCAGACCAAGAAAGATAGACCAACACAAGAA	420
Qy	421	AAGTAA 426	
Db	421	AAAAA 426	

RESULT 11  
 US-09-392-932--9  
 ; Sequence 9, Application US/09392932  
 ; Patent No. 6352975  
 ; GENERAL INFORMATION:

; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; FILE INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-9

Query Match 98.9%; Score 421.2; DB 4; Length 642;  
Best Local Similarity 99.3%; Pred. No. 2.1e-119;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 ATGAATTTCTGCTGCTGTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
DB 1 ATGAATTTCTGCTGCTGTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
  
QY 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
DB 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
  
QY 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCTGTGGAC 180  
DB 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCTGTGGAC 180  
  
QY 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTGCTGCTGCCCTG 240  
DB 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTGCTGCTGCCCTG 240  
  
QY 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCCACTGAGGAGTCC 300  
DB 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCCACTGAGGAGTCC 300  
  
QY 301 AACATCACCATGCAGATTATGCGGATCAAACTTCCAGGCGCAGCAGATAGGAGATG 360  
DB 301 AACATCACCATGCAGATTATGCGGATCAAACTTCCAGGCGCAGCAGATAGGAGATG 360  
  
QY 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
DB 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
  
QY 421 AAGTAA 426  
DB 421 AAAAAA 426

RESULT 12  
US-08-718-904-3  
; Sequence 3, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..657  
; OTHER INFORMATION: /product= "VEGF189-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= "leader sequence-encoding DNA"  
US-08-718-904-3

Query Match 98.9%; Score 421.2; DB 3; Length 677;  
Best Local Similarity 99.3%; Pred. No. 2.1e-119;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 ATGAATTTCTGCTGCTGTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
DB 13 ATGAATTTCTGCTGCTGTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 72  
  
QY 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
DB 73 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 132  
  
QY 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCTGTGGAC 180  
DB 133 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCTGTGGAC 192  
  
QY 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTGCTGCTGCCCTG 240  
DB 193 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTGCTGCTGCCCTG 252  
  
QY 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCCACTGAGGAGTCC 300  
DB 253 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCCACTGAGGAGTCC 312  
  
QY 301 AACATCACCATGCAGATTATGCGGATCAAACTTCCAGGCGCAGCAGATAGGAGATG 360  
DB 313 AACATCACCATGCAGATTATGCGGATCAAACTTCCAGGCGCAGCAGATAGGAGATG 372  
  
QY 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
DB 373 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 432  
  
QY 421 AAGTAA 426  
DB 433 AAAAAA 438

RESULT 13  
PCT-US95-10973A-27  
; Sequence 27, Application PC/TUS9510973A  
; GENERAL INFORMATION:  
; APPLICANT: Prizm Pharmaceuticals, Inc.

**TITLE OF INVENTION:** CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET NUMBER OF CONJUGATES 1.02

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1  TITLE OF INVENTION:  CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
2
3  NUMBER OF SEQUENCES:  107
4
5  CORRESPONDENCE ADDRESS:
6
7  ADDRESSEE:  SEED and BERRY
8
9  STREET:  6300 Columbia Center, 701 Fifth Avenue
10
11 CITY:  Seattle
12
13 STATE:  Washington
14
15 COUNTRY:  USA
16
17 ZIP:  98104-7092
18
19 COMPUTER READABLE FORM:
20
21 MEDIUM TYPE:  Floppy disk
22
23 COMPUTER:  IBM PC compatible
24
25 OPERATING SYSTEM:  PC-DOS/MS-DOS
26
27 SOFTWARE:  PatentIn Release #1.0, Version #1.25
28
29 CURRENT APPLICATION DATA:
30
31 APPLICATION NUMBER:  PCT/US95/10973A
32
33 FILING DATE:  29-AUG-1995
34
35 CLASSIFICATION:
36
37 ATTORNEY/AGENT INFORMATION:
38
39 NAME:  Nottenburg, Carol
40
41 REGISTRATION NUMBER:  39,317
42
43 REFERENCE/DOCKET NUMBER:  760100.413PC
44
45 TELECOMMUNICATION INFORMATION:
46
47 TELEPHONE:  (206) 622-4900
48
49 TELEFAX:  (206) 682-6031
50
51 INFORMATION FOR SEQ ID NO:  27:
52
53 SEQUENCE CHARACTERISTICS:
54
55 LENGTH:  677 base pairs
56
57 TYPE:  nucleic acid
58
59 STRANDEDNESS:  double
60
61 TOPOLOGY:  both
62
63 MOLECULE TYPE:  CDNA
64
65 FEATURE:
66
67 NAME/KEY:  CDS
68
69 LOCATION:  13..657
70
71 OTHER INFORMATION:  /product= "VEGF189-encoding DNA"
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73 FEATURE:
74
75 NAME/KEY:  CDS
76
77 LOCATION:  13..90
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79 OTHER INFORMATION:  /product= "leader sequence-encoding DNA"
80
81 PCT-US95-10973A-27

```

Query Match	98.9%;	Score 421.2;	DB 5;	Length 677;
Best Local Similarity	99.3%;	Pred. No. 2.1e-119;		
Matches 423;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps
QY	1	ATCAACTTTTCGTGCTGCTGGTGCCATTGGAGCCTTGCCTTGCTGCTACCTCCACCAT	60	
Db	13	ATGAAC TTTCGTGCTGCTGGTGCCATTGGAGCCTTGCCTTGCTGCTACCTCCACCAT	72	
QY	61	GCCAAGTGTGCCAGGCTCACCCATTGGCAGAAGGAGGAGCGAGAAATCATCACGAAGTG	120	
Db	73	GCCAAGTGTGCCAGGCTCACCCATTGGCAGAAGGAGGAGCGAGAAATCATCACGAAGTG	132	
QY	121	GTGAAGTTCATGATGCTCTATCAGCGCACCTACTGCCATCCAAATCGAGACCCCTGFTGGAC	180	
Db	133	GTGAAGTTCATGATGCTCTATCAGCGCACCTACTGCCATCCAAATCGAGACCCCTGFTGGAC	192	
QY	181	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTAGACATCTTCAAGCCATCCCTGTGTCGCCCTG	240	
Db	193	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTAGACATCTTCAAGCCATCCCTGTGTCGCCCTG	252	
QY	241	ATGCGGATCGGGGGCTGCTGCAATCAGCAGGCGCTGGAGTGTGTGCCACTCAGGAGTCC	300	
Db	253	ATGCGGATCGGGGGCTGCTGCAATCAGCAGGCGCTGGAGTGTGTGCCACTCAGGAGTCC	312	
QY	301	AACATCACCATCGCATTTATGCGGATCAAACCTCACCAAGGGCCACACATAGGACGAGATG	360	
Db	313	AACATCACCATCGCATTTATGCGGATCAAACCTCACCAAGGGCCACACATAGGACGAGATG	372	
QY	361	AGCTTTCCTACAGCACACAANAATGTGAATCGAGACCAAGAAGAATAGAGCAAGACAAGAA	420	
Db	373	AGCTTTCCTACAGCACACAANAATGTGAATCGAGACCAAGAAGAATAGAGCAAGACAAGAA	432	

QY 421 AAGTAA 426  
|||  
Db 433 AAAAAA 438

RESULT 14

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US-09-392-932-10
; Sequence 10, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS, 002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-392-932-10

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Query Match 98.9%; Score 421.2; DB 4; Length 699;  
Best Local Similarity 99.3%;  
Matches 423; Conservative 0; Mismatches 3; Indels 0;  
Pred. NO. 2.2e-119;

QY	1	ATGAAC	TTTCTGCTGCTTGGGTGCATTTGGAGCCTTTCGCTTGTCTACCTCCACCAT	60
Db	1	ATGAAC	TTTCTGCTGCTTGGGTGCATTTGGAGCCTTTCGCTTGTCTACCTCCACCAT	60
QY	61	GCCAAG	TGTCCTCCAGCGTCACCCATTCGGCAGAGGAGGCGAGAAATCATCAGCAAGT	120
Db	61	GCCAAG	TGTCCTCCAGCGTCACCCATTCGGCAGAGGAGGCGAGAAATCATCAGCAAGT	120
QY	121	GTGAAG	TTTCATGGATGCTCTATCAGCGCAGCTACTGCGCATCCAAATCGAGACCCCTGGTGGAC	180
Db	121	GTGAAG	TTTCATGGATGCTCTATCAGCGCAGCTACTGCGCATCCAAATCGAGACCCCTGGTGGAC	180
QY	181	ATCTTC	CCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCATTCCTGTGTGCCCTTG	240
Db	181	ATCTTC	CCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCATTCCTGTGTGCCCTTG	240
QY	241	ATGCGAT	CGGGGGCTGCTGCTCAATGACGAGGCGCTTGGAGTGTGCCCACTCAGAGATCC	300
Db	241	ATGCGAT	CGGGGGCTGCTGCTCAATGACGAGGCGCTTGGAGTGTGCCCACTCAGAGATCC	300
QY	301	ACATC	CACCATCGAGATTATCGGGATCAAACTCCAAAGGCCAGCACATAGGAGAGATG	360
Db	301	ACATC	CACCATCGAGATTATCGGGATCAAACTCCAAAGGCCAGCACATAGGAGAGATG	360
QY	361	AGCTTC	TCTACAGCAACAATAATGTGAATCGACACCAAGAAAGATAGACCAAGACAAGNA	420
Db	361	AGCTTC	TCTACAGCAACAATAATGTGAATCGACACCAAGAAAGATAGACCAAGACAAGAA	420
QY	421	AAGTAA	426	
Db	421	AAAAAA	426	

## RESULT 15

US-08-718-904-4  
; Sequence 4, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.

Query Match	98.9%	Score	421.2	DB	3	Length	728
Best Local Similarity	99.3%	Pred.	No. 2.2e-119				
Matches	423	Conservative	0	Mismatches	3	Indels	0
QY	1	ATCAACTTTCTGCTGTCCTTGGGTGCATTGGAGCCTTGCCCTTGCTGCTCTACCTCCACCAT	60				
Db	13	ATGAACCTTCTGCTGTCCTTGGGTGCATTGGAGCCTTGCCCTTGCTGCTCTACCTCCACCAT	72				
QY	61	GCCAAAGTGTCACAGGCTGCACCCATGGCAGAAGGAGGGCAGAAATCATCAGGAAGTG	120				
Db	73	GCCAAAGTGTCACAGGCTGCACCCATGGCAGAAGGAGGGCAGAAATCATCAGGAAGTG	132				
QY	121	GTCAAGTTTCATGATGTCATACAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC	180				
Db	133	GTGAAGTTTCATGATGTCATACAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC	192				
QY	181	ATCTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGT	240				
Db	193	ATCTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGT	252				
QY	241	ATCGGATCGGGGGCTGCTCCATGACGAGGGCCTGAGTGTGTGCCCATGAGGATCC	300				
Db	253	ATCGGATCGGGGGCTGCTCCATGACGAGGGCCTGAGTGTGTGCCCATGAGGATCC	312				
QY	301	AAGATCACCATTGCAGATTATGCGGATCAAACTCACCAGGCCACGACATAGGAGAGATG	360				
Db	313	AACATCACCATTGCAGATTATGCGGATCAAACTCACCAGGCCACGACATAGGAGAGATG	372				
QY	361	AGCTTCCTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAACAGAA	420				
Db	373	AGCTTCCTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAACAGAA	432				

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 04:57:39 ; Search time 28 Seconds  
(without alignments)  
148.165 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWVHWSLALLYLHH.....FLQHNKCEPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	792	100.0	147	3	US-08-807-992B-1
2	792	100.0	147	4	US-09-392-932-1
3	792	100.0	147	4	US-08-706-054A-4
4	792	100.0	214	6	5240848-11
5	792	100.0	215	3	US-08-807-992B-3
6	792	100.0	215	4	US-08-586-039B-49
7	792	100.0	215	6	5240848-7
8	792	100.0	232	2	US-08-999-811-7
9	792	100.0	232	2	US-08-824-996-9
10	792	100.0	232	3	US-08-807-992B-4
11	792	100.0	232	3	US-09-042-105-7
12	787	99.4	191	3	US-08-567-200A-2
13	787	99.4	191	3	US-08-807-992B-2
14	787	99.4	191	3	US-08-691-794-2
15	787	99.4	191	4	US-08-795-430-56
16	787	99.4	191	4	US-09-392-932-3
17	787	99.4	191	4	US-09-355-700-56
18	787	99.4	191	4	US-08-882-816-2
19	787	99.4	191	6	5332671-4
20	773.5	97.7	231	5	PCT-US96-090001-10
21	766	96.7	215	6	5219739-22
22	717.5	90.6	190	6	5332671-3
23	685.5	86.6	146	4	US-08-586-039B-33
24	685.5	86.6	214	4	US-08-586-039B-35
25	680.5	85.9	190	4	US-08-586-039B-31
26	672.5	84.9	190	2	US-08-569-063C-20
27	653	82.4	189	1	US-08-469-427A-15

28	645	81.4	121	6	5194596-19	Patent No. 5194596
29	645	81.4	121	6	5219739-20	Patent No. 5219739
30	645	81.4	145	3	US-08-784-551C-2	Sequence 2, Appl
31	645	81.4	145	4	US-09-392-932-2	Sequence 2, Appl
32	640	80.8	165	4	US-08-882-816-3	Sequence 3, Appl
33	640	80.8	165	6	5194596-18	Patent No. 5194596
34	640	80.8	165	6	5219739-19	Patent No. 5219739
35	621	78.4	110	4	US-09-392-932-11	Sequence 11, Appl
36	616	77.8	109	3	US-08-691-794-3	Sequence 3, Appl
37	575.5	72.7	120	6	5194596-9	Patent No. 5194596
38	575.5	72.7	120	6	5219739-9	Patent No. 5219739
39	570.5	72.0	164	6	5194596-17	Patent No. 5194596
40	570.5	72.0	164	6	5219739-17	Patent No. 5219739
41	570.5	72.0	164	6	5219739-18	Patent No. 5219739
42	325	41.0	149	1	US-08-469-427A-14	Sequence 14, Appl
43	325	41.0	149	2	US-08-039-297B-2	Sequence 2, Appl
44	325	41.0	149	2	US-08-569-063C-21	Sequence 21, Appl
45	325	41.0	149	4	US-08-795-430-55	Sequence 55, Appl

## ALIGNMENTS

## RESULT 1

US-08-807-992B-1

; Sequence 1, Application US/08807992B

; Patent No. 6022541

; GENERAL INFORMATION:

; APPLICANT: Senger, Donald R

; APPLICANT: Dvorak, Harold F

; TITLE OF INVENTION: Immunological preparation for concurrent

; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular

; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blo

; TITLE OF INVENTION: vessel

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David Prashker, Esq.

; STREET: P.O. Box 5387

; CITY: Magnolia

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 01930

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

; COMPUTER: IBM PS/1

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Wordperfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/807,992B

; FILING DATE: March 3, 1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: David Prashker, Esq.

; REGISTRATION NUMBER: 29,693

; REFERENCE/DOCKET NUMBER: BIS-033

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (978) 525-3794

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 147 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-807-992B-1

Query Match

Best Local Similarity 100.0%; Score 792; DB 3; Length 147;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHHAKWSQAPMAEGGQNNHHEVVKFMDVYORSYCHPIETLVD 60

Db 1 MNFLSWVHWSLALLYLHHAKWSQAPMAEGGQNNHHEVVKFMDVYORSYCHPIETLVD 60

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QY 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
Db 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
QY 121 SFLOHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLOHNKCECRPKKDRARQEK 141
|||||
RESULT 2
US-09-392-932-1
; Sequence 1, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-392-932-1

Query Match 100.0%; Score 792; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
|||||
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QY 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
Db 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
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QY 121 SFLOHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLOHNKCECRPKKDRARQEK 141
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RESULT 3
US-08-706-054A-4
; Sequence 4, Application US/08706054A
; Patent No. 6451764
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: VEGF-Related Protein
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,054A
; FILING DATE: 30-Aug-1996
; CLASSIFICATION: <unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/003491
; FILING DATE: 08-Sep-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0963R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-706-034A-4

Query Match 100.0%; Score 792; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
|||||
Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
|||||
QY 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
Db 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
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QY 121 SFLOHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLOHNKCECRPKKDRARQEK 141
|||||
RESULT 4
5240848-11
; Patent No. 5240848
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/337,037
; FILING DATE: 10-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 274,061
; FILING DATE: 21-NOV-1988
; SEQ ID NO: 11:
; LENGTH: 214
5240848-11

Query Match 100.0%; Score 792; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.3e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
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Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
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QY 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
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Db 61 IFQEPDEIYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120
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Db 121 SFLOHNKCECRPKKDRARQEK 141
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RESULT 5
US-08-807-992B-3
; Sequence 3, Application US/08807992B
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Patent No. 6022541  
GENERAL INFORMATION:  
APPLICANT: Senger, Donald R  
APPLICANT: Dvorak, Harold F  
TITLE OF INVENTION: Immunological preparation for concurrent  
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
TITLE OF INVENTION: vessel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WordPerfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/807,992B  
FILING DATE: March 3, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-807-992B-3  
Query Match 100.0%; Score 792; DB 3; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 6  
US-08-586-039B-49  
Sequence 49, Application US/08586039B  
Patent No. 6140073  
GENERAL INFORMATION:  
APPLICANT: Bayne, Marvin L.  
APPLICANT: Thomas Jr., Kenneth A.  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C  
SUBUNIT  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0900

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,039B  
FILING DATE: 16-JAN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/124,259  
FILING DATE: 20-SEP-1993  
APPLICATION NUMBER: 07/676,436  
FILING DATE: 28-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18361DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-586-039B-49  
Query Match 100.0%; Score 792; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 7  
5240848-7  
Patent No. 5240848  
APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH  
TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR  
PERMEABILITY FACTOR HAVING 189 AMINO ACIDS  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/337,037  
FILING DATE: 10-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 274,061  
FILING DATE: 21-NOV-1988  
SEQ ID NO: 7  
LENGTH: 215  
5240848-7  
Query Match 100.0%; Score 792; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLLSWVHSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120

Db 61 IFOEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 8  
US-08-999-811-7  
; Sequence 7, Application US/08999811  
; Patent No. 5932540  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 NEW YORK AVENUE  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/999,811  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,550  
; FILING DATE: 8-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MARKOWICZ, KAREN R.  
; REGISTRATION NUMBER: 36,351  
; REFERENCE/DOCKET NUMBER: 1488.1000004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
US-08-999-811-7

Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNNHVEYVKFMDVYQSYCHPIETLVD 60  
QY 61 IFOEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
Db 61 IFOEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 9

US-08-824-996-9  
; Sequence 9, Application US/08824996B  
; Patent No. 5935820  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth  
; TITLE OF INVENTION: Factor 2  
; FILE REFERENCE: PF11201  
; CURRENT APPLICATION NUMBER: US/08/824,996B  
; CURRENT FILING DATE: 1997-03-27  
; EARLIER APPLICATION NUMBER: 08/207,550  
; EARLIER FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-824-996-9  
Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNNHVEYVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNNHVEYVKFMDVYQSYCHPIETLVD 60  
QY 61 IFOEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
Db 61 IFOEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGQHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 10  
US-08-807-992B-4  
; Sequence 4, Application US/08807992B  
; Patent No. 6022541  
; GENERAL INFORMATION:  
; APPLICANT: Senger, Donald R  
; APPLICANT: Dvorak, Harold F  
; TITLE OF INVENTION: Immunological preparation for concurrent  
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bio  
; TITLE OF INVENTION: vessel  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David Prashker, Esq.  
; STREET: P.O. Box 5387  
; CITY: Magnolia  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01930  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
; COMPUTER: IBM PS/1  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,992B  
; FILING DATE: March 3, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David Prashker, Esq.  
; REGISTRATION NUMBER: 29,693  
; REFERENCE/DOCKET NUMBER: BIS-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (978) 525-3794

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-807-992B-4

Query Match 100.0%; Score 792; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
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DB 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
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QY 61 IFOEYPDEIEYIFKSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
|||||  
DB 61 IFOEYPDEIEYIFKSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
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QY 121 SFLQHNKCECRPKKDRARQEK 141  
|||||  
DB 121 SFLQHNKCECRPKKDRARQEK 141  
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RESULT 11  
US-09-042-105-7  
; Sequence 7, Application US/09042105  
; Patent No. 6040157  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 NEW YORK AVENUE  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042.105  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,550  
; FILING DATE: 8-MAR-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,968  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: TO BE ASSIGNED  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERIC K. STEFFE  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-09-042-105-7

Query Match 100.0%; Score 792; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
|||||  
DB 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
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QY 61 IFOEYPDEIEYIFKSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
|||||  
DB 61 IFOEYPDEIEYIFKSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRIKPHQGQHIGEM 120  
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QY 121 SFLQHNKCECRPKKDRARQEK 141  
|||||  
DB 121 SFLQHNKCECRPKKDRARQEK 141  
|||||

RESULT 12  
US-08-567-200A-2  
; Sequence 2, Application US/08567200A  
; Patent No. 6020473  
; GENERAL INFORMATION:  
; APPLICANT: Keyt, Bruce A.  
; APPLICANT: Nguyen, Francis H.  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: Variants of Vascular Endothelial Cell  
; TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their  
; TITLE OF INVENTION: Production  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/567.200A  
; FILING DATE: 05-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-62326-1/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-567-200A-2

Query Match 99.4%; Score 787; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
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Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

RESULT 13  
US-08-807-992B-2  
; Sequence 2, Application US/08807992B  
; Patent No. 6022541  
; GENERAL INFORMATION:  
; APPLICANT: Senger, Donald R  
; APPLICANT: Dvorak, Harold F  
; TITLE OF INVENTION: Immunological preparation for concurrent  
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David Prashker, Esq.  
; STREET: P.O. Box 5387  
; CITY: Magnolia  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01930  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
; COMPUTER: IBM PS/1  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Wordperfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,992B  
; FILING DATE: March 3, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David Prashker, Esq.  
; REGISTRATION NUMBER: 29,693  
; REFERENCE/DOCKET NUMBER: BIS-033  
; TELEPHONE: (978) 525-3794  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-807-992B-2

Query Match 99.4%; Score 787; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

RESULT 14  
US-08-691-794-2  
; Sequence 2, Application US/08691794

; Patent No. 6057428  
; GENERAL INFORMATION:  
; APPLICANT: Keyt, Bruce A.  
; APPLICANT: Nguyen, Francis H.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Cunningham, Brian C.  
; APPLICANT: Wells, James A.  
; APPLICANT: Li, Bing  
; TITLE OF INVENTION: Variants of Vascular Endothelial Cell  
; TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,794  
; FILING DATE: 02-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/002,827  
; FILING DATE: 25-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/567,200  
; FILING DATE: 05-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63758/WH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-691-794-2

Query Match 99.4%; Score 787; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEYDPELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

RESULT 15  
US-08-795-430-56  
; Sequence 56, Application US/08795430  
; Patent No. 6130071  
; GENERAL INFORMATION:  
; APPLICANT: Alicalo, Karl

Job time : 30 secs

APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/795,430  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-430-56

Query Match 99.4%; Score 787; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MNLLSWHWSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD	60
Qy	61	IFQEYPDEIEYIFKPCVPLMRCGCCNDGLEGCVPTESNITMQIMRIKPHQGQIHGM	120
Db	61	IFQEYPDEIEYIFKPCVPLMRCGCCNDGLEGCVPTESNITMQIMRIKPHQGQIHGM	120
Qy	121	SFLQHNKCECRPKDRARQE	140
Db	121	SFLQHNKCECRPKDRARQE	140

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 05:02:33 ; Search time 56 Seconds

(without alignments)  
772.168 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLLSVWHSALLLLYHH.....FLOHNKCECRPKDRARQEK 141

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Xgapop 10.0 , Xgapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	444	4	US-09-392-932-6
2	792	100.0	473	3	US-08-718-904-1
3	792	100.0	473	5	PCT-US95-10973A-25
4	792	100.0	516	3	US-08-784-551C-1
5	792	100.0	642	4	US-09-392-932-9
6	792	100.0	648	3	US-08-586-039B-48
7	792	100.0	677	3	US-08-718-904-3
8	792	100.0	677	5	PCT-US95-10973A-27
9	792	100.0	699	4	US-09-392-932-10
10	792	100.0	728	3	US-08-718-904-4
11	792	100.0	728	5	PCT-US95-10973A-28
12	792	100.0	774	3	US-08-765-340-1

13	792	100.0	1195	6	5240848-6	Patent No. 5240848
14	792	100.0	1212	5	PCT-US95-10973A-31	Sequence 31, Appl
15	787	99.4	576	4	US-09-392-932-8	Sequence 8, Appl
16	787	99.4	605	3	US-08-718-904-2	Sequence 2, Appl
17	787	99.4	605	5	PCT-US95-10973A-26	Sequence 26, Appl
18	787	99.4	989	6	5332671-11	Patent No. 5332671
19	787	99.4	990	3	US-08-567-200A-1	Sequence 1, Appl
20	787	99.4	990	3	US-08-691-794-1	Sequence 1, Appl
21	787	99.4	990	4	US-08-882-816-1	Sequence 1, Appl
22	787	99.4	1369	5	PCT-US95-10973A-33	Sequence 33, Appl
23	783	98.9	516	4	US-09-392-932-7	Sequence 7, Appl
24	781.5	98.7	456	5	PCT-US95-10973A-88	Sequence 88, Appl
25	781.5	98.7	467	5	PCT-US95-10973A-86	Sequence 86, Appl
26	776.5	98.0	599	5	PCT-US95-10973A-87	Sequence 87, Appl
27	776.5	98.0	599	5	PCT-US95-10973A-89	Sequence 89, Appl
28	717.5	90.6	1543	6	5332671-5	Patent No. 5332671
29	685.5	86.6	445	3	US-08-586-039B-32	Sequence 32, Appl
30	685.5	86.6	649	3	US-08-586-039B-34	Sequence 34, Appl
31	680.5	85.9	573	3	US-08-586-039B-30	Sequence 30, Appl
32	657	83.0	886	6	5219739-23	Patent No. 5219739
33	656.5	82.9	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
34	656.5	82.9	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
35	651.5	82.3	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	649.5	82.0	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
37	640	80.8	498	6	5194596-20	Patent No. 5194596
38	640	80.8	498	6	5219739-21	Patent No. 5219739
39	640	80.8	1269	5	PCT-US95-10973A-32	Sequence 32, Appl
40	570.5	72.0	961	6	5219739-16	Patent No. 5219739
41	562.5	71.0	961	6	5194596-16	Patent No. 5194596
42	525	66.3	789	6	5219739-8	Patent No. 5219739
43	525	66.3	790	6	5194596-8	Patent No. 5194596
44	366	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	325	41.0	450	3	US-08-586-039B-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-392-932-6  
; Sequence 6, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-6

Alignment Scores:	Pred. No.:	Score:	5:38e-93	Length:	444
Percent Similarity:	792.00	100.00%	Matches:	141	
Best Local Similarity:	100.00%	Conservative:	0		
Query Match:	100.00%	Mismatches:	0		
DB:	4	Indels:	0		
		Gaps:	0		

US-09-884-050-2 (1-141) x US-09-392-932-6 (1-444)

Qy 1 MetAsnPhLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrlHuHisHis 20  
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Db 1 ATGAACCTTCTGCTGCTTGGGTGCATTGGAGCCCTTGCCTTACCTCCACCAT 60







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QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
DB 361 AGCTTCTACGACACAAATGTGAATGATGAGACCAAGAAAGATAGACGACAGCAAGAA 420
QY 141 Lys 141
DB 421 AAA 423
RESULT 5
US-09-392-932-9
; Sequence 9, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-392-932-9
Alignment Scores:
Pred. No.: 9,12e-93 Length: 642
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-884-050-2 (1-141) x US-09-392-932-9 (1-642)
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20
DB 1 ATGAATTTCTGCTGCTGTGGTGCAATGGAGCCTCGCCTTGCTGCTCTACCTCCACCAT 60
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
DB 61 GCCAAGTGGTCCAGCTGCACCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
DB 121 GTCAAGTTCATGGATGCTATACGCGCAGCTACTGCCATCCATCGAGACCCCTGGTGGAC 180
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
DB 181 ATCTTCAGAGGTACCTCATGATGATCGATGATCATCTTCAAGCCATCCGTGTGCCCCCTG 240
QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
DB 241 ATCGGATGCGGGGCTGCTGCAATGACGAGGGGCTGGAGTGTGTGCCACTGAGGAGTCC 300
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
DB 301 AACATCACCATGCGAGATTATGCGGATCAACACCTTCACCAAGGCCAGCACATAGAGAGATG 360
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
DB 361 AGCTTCTACGACACAAATGTGAATGATGAGACCAAGAAAGATAGACGACAGCAAGAA 420
QY 141 Lys 141
DB 421 AAA 423
RESULT 6
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US-08-586-039B-48
; Sequence 48, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..648
US-08-586-039B-48
Alignment Scores:
Pred. No.: 9,24e-93 Length: 648
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-884-050-2 (1-141) x US-08-586-039B-48 (1-648)
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20
DB 1 ATGAATTTCTGCTGCTGTGGTGCAATGGAGCCTTGCTGCTCTACCTCCACCAT 60
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
DB 61 GCCAAGTGGTCCAGCTGCACCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
DB 121 GTGAAGTTCATGGATGCTATACGCGCAGCTACTGCCATCCATCGAGACCCCTGGTGGAC 180
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
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Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATGCCATCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGAGTCC 300  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGCAGATTATGGGATCAACCTCACCAGGCCAGCACATAGGAGATG 360  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGAA 420  
Qy 141 Lys 141  
Db 421 AAA 423

RESULT 7  
US-08-718-904-3  
; Sequence 3, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..657  
; OTHER INFORMATION: /product= "VEGF189-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= "leader sequence-encoding DNA"

US-08-718-904-3  
Alignment Scores:  
Pred. No.: 9,83e-93 Length: 677  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0  
US-09-884-050-2 (1-141) x US-08-718-904-3 (1-677)  
Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTyrLeuHisHis 20  
Db 13 ATGAACCTTCTGCTGCTTGGTGCATTTGGAGCCTTGCTTGTCTGTCTACCTCCACCAT 72  
Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
Db 73 GCCAAGTGGTCCAGCTGCACCCATGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 132  
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 133 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCATGAGACCCCTGTGGAC 192  
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 193 ATCTTCCAGGAGTACCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 252  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 253 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTGCCACTGAGGAGTCC 312  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 313 AACATCACCATGCAGATTATGGGATCAACCTCACCAGGCCAGCACATAGGAGATG 372  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 373 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGAA 432  
Qy 141 Lys 141  
Db 433 AAA 435

RESULT 8  
PCT-US95-10973A-27  
; Sequence 27, Application PC/TUS9510973A  
; GENERAL INFORMATION:  
; APPLICANT: Prizm Pharmaceuticals, Inc.  
; TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGE  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/10973A  
; FILING DATE: 29-AUG-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nottenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.413PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both







Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyMet 120  
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 Db 457 AACATCACCATGCAGATTATCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 516  
 |||||  
 Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 |||||  
 Db 517 AGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 576  
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 Qy 141 Lys 141  
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 Db 577 AAA 579

## RESULT 14

PCT-US95-10973A-31  
 ; Sequence 31, Application PC/TUS9510973A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Prizm Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED and BERRY  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/10973A  
 ; FILING DATE: 29-AUG-1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Nottenburg, Carol  
 ; REGISTRATION NUMBER: 39,317  
 ; REFERENCE/DOCKET NUMBER: 760100.413PC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1212 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 4..1212  
 ; OTHER INFORMATION: /product= "VEGF121-SAP LEADER"  
 ; OTHER INFORMATION: p21B"  
 ; NAME/KEY: CDS  
 ; LOCATION: 4..81  
 ; OTHER INFORMATION: /product= "LEADER"  
 PCT-US95-10973A-31

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 Pred. No.: 2.26e-92 Length: 1212  
 Score: 792.00 Matches: 141  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

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Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
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 Db 64 GCCAAGTGTCCAGGCTGCACCAATGCGACAAGAGAGAGGCGAGAATCATCACGAAGTG 123  
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 Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
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 Db 124 GTGAAGTTTCATGGATGTCTATCAGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 183  
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Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
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 Db 184 ATCTTCCAGGAGTAGCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTGCCCTG 243  
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Qy 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 |||||  
 Db 244 ATGCGATCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTCCACTGAGGAGTCC 303  
 |||||

Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 |||||  
 Db 304 AACATCACCATGCAGATTATGCGATCAAACTCACCAGGCCAGCACATAGGAGATG 363  
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Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
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 Db 364 AGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 423  
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Qy 141 Lys 141  
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Db 424 AAA 426

## RESULT 15

US-09-392-932-8  
 ; Sequence 8, Application US/09392932  
 ; Patent No. 6352975  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schreiner, George F.  
 ; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
 ; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
 ; FILE REFERENCE: SCIOS.002A  
 ; CURRENT APPLICATION NUMBER: US/09/392,932  
 ; CURRENT FILING DATE: 1999-09-09  
 ; EARLIER APPLICATION NUMBER: 60/099,694  
 ; EARLIER FILING DATE: 1998-09-09  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 576  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-09-392-932-8

Alignment Scores:  
 Pred. No.: 3.43e-92 Length: 576  
 Score: 787.00 Matches: 140  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.37% Indels: 0  
 DB: 4 Gaps: 0

US-09-884-050-2 (1-141) x US-09-392-932-8 (1-576)

Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
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 Db 1 ATGAACCTTCTGCTCTTGGTGATTTGGAGCCCTTGCCTTGCCTTACCTCCACCAT 60  
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Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
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 Db 61 GCCAAGTGTCCAGGCTGCACCAATGCGACAAGAGAGAGGCGAGAATCATCACGAAGTG 120  
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Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
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 Db 121 GTGAAGTTTCATGGATGTCTATCAGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 180  
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QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
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Db 181 ATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240  
QY 81 MetArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
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Db 241 ATCGATGCGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
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Db 301 AACATCACCATGCGAGATTATGCGGATCAAACTCACCAAGGCCAGCACATAGGAGAGATG 360  
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Search completed: November 20, 2002, 06:31:38  
Job time : 68 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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3475.910 Million cell updates/sec

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24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	99.8	495	AAZ29996	Nucleotide sequenc
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3	422.8	99.2	516	AAV28396	Vascular endotheli
4	422.8	99.2	545	AAZ29999	Nucleotide sequenc
5	422.8	99.2	648	AAZ39835	Human A215 nucleot
6	422.8	99.2	648	AAZ39835	Human VEGF C subun
7	422.8	99.2	666	AAZ29998	Nucleotide sequenc
8	422.8	99.2	1195	AAQ04474	Human vascular per
9	422.8	99.2	1195	AAZ90498	Human vascular end

10	422.4	99.2	444	21	AAZ93345	Human vascular end
11	422.4	99.2	444	21	AAZ99544	Nucleotide sequenc
12	422.4	99.2	444	22	AAC90473	Human vascular end
13	422.4	99.2	444	22	AAC90477	Human VEGF121 DNA
14	422.4	99.2	444	24	ABL57427	Human vascular end
15	422.4	99.2	473	15	AAQ99080	cDNA encoding huma
16	422.4	99.2	473	17	AAT17613	VEGF121 coding seq
17	422.4	99.2	473	17	AAAT12853	cDNA encoding VEGF
18	422.4	99.2	544	22	AAT21876	Human VEGF splice
19	422.4	99.2	774	18	AAT85644	Antisense inhibito
20	422.4	99.2	774	18	AAT79139	Human vascular end
21	422.4	99.2	774	19	AAV15102	Human vascular end
22	422.4	99.2	774	19	AAV15103	Human vascular end
23	422.4	99.2	1873	19	AAV15103	Human vascular end
24	422.4	99.2	1873	20	AAH21568	Vascular endotheli
25	422	99.1	541	22	AAH26082	Vascular endotheli
26	422	99.1	573	22	AAH24900	Nucleotide sequenc
27	422	99.1	576	24	AAH31056	Human vascular end
28	422	99.1	576	24	ABL91778	Human polynucleoti
29	422	99.1	605	16	AAQ99081	cDNA encoding huma
30	422	99.1	605	17	AAT17614	VEGF165 coding seq
31	422	99.1	605	21	AAAT12854	cDNA encoding VEGF
32	422	99.1	649	17	AAT33609	Vascular endotheli
33	422	99.1	1395	17	AAT35740	VEGF165-Alamet-SAP
34	422	99.1	4597	22	AAF24901	Nucleotide sequenc
35	422	99.1	5610	21	AAH75628	Nucleotide sequenc
36	422	99.1	5610	24	AAD39240	pD10-VEGFuc vector
37	421.2	98.9	516	20	AAH57724	Human VEGF(145) co
38	421.2	98.9	516	21	AAZ93346	Human vascular end
39	421.2	98.9	516	21	AAZ99545	Nucleotide sequenc
40	421.2	98.9	516	22	AAC90478	Human VEGF145 DNA
41	421.2	98.9	516	24	ABL57428	Human vascular end
42	421.2	98.9	642	21	AAZ93348	Human vascular end
43	421.2	98.9	642	21	AAZ99547	Nucleotide sequenc
44	421.2	98.9	642	22	AAC90480	Human VEGF189 DNA
45	421.2	98.9	642	24	ABL57430	Human vascular end

ALIGNMENTS

RESULT 1

AAZ29996  
ID AAZ29996 standard; cDNA; 495 BP.

XX AC AAZ29996;

XX XX 26-JAN-2000 (first entry)

DT XX Nucleotide sequence of VEGF-Al38 protein coding region.

DE XX Vascular endothelial factor; VEGF; VEGF-Al38: variant; vascular disease;  
KW cardiovascular disease; vascular cell proliferation; angioplasty;  
KW restenosis; drug permeation; tumour; ischemic condition;  
KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
KW chronic lower limb ischemia; peripheral vascular disease; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..495

FT FT /\*tag= a

FT FT /product= "VEGF-Al38"

FT FT sig\_peptide 1..78

FT FT /\*tag= b

FT FT /note= "secretion signal sequence"

FT FT exon 1..90

FT FT /\*tag= c

FT FT /number= 1

FT FT exon 91..118

FT FT /\*tag= d

FT FT /number= 2

FT FT exon 119..315





CC	infarction, chronic coronary ischemia, chronic lower limb ischemia, stroke and peripheral vascular disease. In addition they may be used to treat wounds.	
CC		
CC		
XX		
SQ	Sequence 545 BP; 160 A; 131 C; 152 G; 102 T; 0 other;	
	Query Match 99.2%; Score 422.8; DB 20; Length 545;	
	Best Local Similarity 99.5%; Pred. No. 5.3e-118;	
	Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCGCTTGCCCTTGCTGCTCTACCTCCACCAT 60	
DB	13 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCGCTTGCCCTTGCTGCTCTACCTCCACCAT 72	
QY	61 GCCAAGTGGTCCCAAGGCTGCACCCATGGCAGAGGAGGGGCGAGAATCATCAGCAAGTG 120	
DB	73 GCCAAGTGGTCCCAAGGCTGCACCCATGGCAGAGGAGGGGCGAGAATCATCAGCAAGTG 132	
QY	121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 180	
DB	133 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 192	
QY	181 ATCTTCAGAGTAGTACCTGATGAGATCGATACATCTTCAAGCCATCCTGTGTGCCCTG 240	
DB	193 ATCTTCAGAGTAGTACCTGATGAGATCGATACATCTTCAAGCCATCCTGTGTGCCCTG 252	
QY	241 ATCGGATGCGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGTGCCCTGAGGAGTCC 300	
DB	253 ATCGGATGCGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGTGCCCTGAGGAGTCC 312	
QY	301 AACATCACCATGTCAGATTATGCGGATCAAACTCACCAGGCCAGCATAGGAGAGATG 360	
DB	313 AACATCACCATGTCAGATTATGCGGATCAAACTCACCAGGCCAGCATAGGAGAGATG 372	
QY	361 AGCTTCTACAGCACACAATGTGAATGCAGACCAAGAAGATAGAGCAAGACAAGAA 420	
DB	373 AGCTTCTACAGCACACAATGTGAATGCAGACCAAGAAGATAGAGCAAGACAAGAA 432	
QY	421 AAGTAA 426	
DB	433 AAAAA 438	
RESULT 5		
AAZ39835		
ID	AAZ39835 standard; cDNA; 648 BP.	
XX		
XX	AAZ39835;	
XX		
XX		
XX	15-FEB-2000 (first entry)	
XX		
XX	Human A215 nucleotide sequence.	
XX		
XX	VEGF; vascular endothelial growth factor; C subunit; tissue growth; A217;	
KW	vascular development; artificial blood vessel; repair; human; ss.	
KW		
OS	Homo sapiens.	
XX		
XX		
Key	Location/Qualifiers	
FT	1..648	
CDS	/*tag= a	
FT	/product= A215	
FT		
XX		
XX	U55994300-A.	
PN		
XX		
XX	30-NOV-1999.	
XX		
XX	20-SEP-1993; 93US-0124259.	
XX		
XX	28-MAR-1991; 91US-0676436.	
XX		
XX	(MERI ) MERCK & CO INC.	











[illegible]

each comprising at least amino acids 11-116 of a defined 147 amino acid sequence, or a sequence having at least 90% identity to the defined sequence, and retaining a cysteine at or corresponding to position 116, which is disulphide-bonded to an additional extraneous cysteine. The VEGF dimer is useful for inducing angiogenesis and vascular remodelling, treating peripheral arterial disease, coronary artery disease, essential hypertension, microvascular angioopathy and polycystic kidney disease, and repair of vascular endothelial cell layers. It is also useful for treating injuries, wounds, hypoxia, hypercapnia, pulmonary dysfunction, kidney diseases, diseases arising from disordered transport of solutes and fluids across the intestinal epithelium including inflammatory bowel disease, and disorders due to accumulation of ascites in the peritoneum.

Sequence 444 BP: 121 A: 113 C: 122 G: 88 T: 0 other: 0

Query Match 99.2%; Score 422.4; DB 22; Length 444;  
Best Local Similarity 99.8%; Pred. No. 6.4e-118;  
Matches 423: Conservative 0; Mismatches 1; Indels 0;

0.

[illegible]

RESULT 13

REC'D 10  
AAC90477  
ID AAC90477 standard: DNA: 444 BP.

AAC90477:

DT 13-MAR-2001 (first entry)

XX DE Human VEGF121 DNA.

XX Human; VEGF; vascular endothelial growth factor; VEGF121; VEGF145;  
KW cardant; cerebroprotective; hypotensive; nephrotropic; antidiabetic;  
KW dermatological; immunosuppressive; antiinflammatory; cytostatic;  
KW vasotrophic; antibacterial; angiogenesis; vascular remodelling;  
KW vascular disease; kidney disease; diabetes; systemic lupus erythematosus;  
KW meningitis; tumour; infection; lung disease inflammatory bowel disease;  
KW as

XX  
OS  
Homo sapiens.

XX 33 FOLIO 2

100

23

PN XX PD XX PF XX PR XX PA XX PI XX DR DR XX PT PT PT PT

Query Match 99.28: Score 422.4: DB 22: Length 444:

0.

[illegible]

Sequence 444 BP: 121 A; 113 C; 122 G; 88 T; 0 other;

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Query Match      99.2%; Score 422.4; DB 22; Length 444;
Best Local Similarity 99.8%; Pred. No. 6.4e-118;
Matches 423: Conservative 0; Mismatches 1; Indels 0;
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[illegible]





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 20, 2002, 01:17:26 ; Search time 2685 Seconds  
(without alignments)  
4617.428 Million cell updates/sec

Title: US-09-884-050-1  
Perfect score: 426  
Sequence: 1 atgaactttctgtctgttg.....gagcaagacaagaaagtaa 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_un.\*
- 28: em\_vl.\*
- 29: em\_vt.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	422.8	99.2	630	9 HSA010438	AJ010438 Homo sapi
2	422.8	99.2	648	6 AR117116	AR117116 Sequence
3	422.8	99.2	1195	9 HUMVDP	M27281 Human vascu
4	422.4	99.2	444	6 AR198591	AR198591 Sequence
5	422.4	99.2	444	6 AX048686	AX048686 Sequence
6	422.4	99.2	444	6 AX050391	AX050391 Sequence
7	422.4	99.2	444	6 AF214570	AF214570 Homo sapi
8	422.4	99.2	544	6 E49139	E49139 Human large
9	422.4	99.2	774	6 AR118875	AR118875 Sequence
10	422.4	99.2	774	6 E11017	E11017 A part of p
11	422.4	99.2	774	6 E13215	E13215 Human mRNA
12	422.4	99.2	774	6 E13325	E13325 cDNA encod1
13	422.4	99.2	774	6 E14233	E14233 Human mRNA
14	422.4	99.2	774	6 E15156	E15156 Human VEGF
15	422.4	99.2	1873	6 E15157	E15157 Human VEGF
16	422.4	99.2	1873	6 E22645	E22645 Antisense n
17	422.4	99.1	541	6 AX204783	AX204783 Sequence
18	422.4	99.1	541	9 AF091352	AF091352 Homo sapi
19	422.4	99.1	573	6 AX060342	AX060342 Sequence
20	422.4	99.1	576	6 AX481507	AX481507 Sequence
21	422.4	99.1	576	9 AB021221	AB021221 Homo sapi
22	422.4	99.1	576	9 AF486837	AF486837 Homo sapi
23	422.4	99.1	606	9 AF430806	AF430806 Homo sapi
24	422.4	99.1	649	9 HSVEGF	X62568 H. sapiens v
25	422.4	99.1	4597	6 AX060344	AX060344 Sequence
26	422.4	99.1	5610	6 AX411805	AX411805 Sequence
27	421.2	98.9	516	6 AR198592	AR198592 Sequence
28	421.2	98.9	516	6 AX029451	AX029451 Sequence
29	421.2	98.9	516	6 AX050393	AX050393 Sequence
30	421.2	98.9	642	6 AR198594	AR198594 Sequence
31	421.2	98.9	642	6 AX050397	AX050397 Sequence
32	421.2	98.9	699	6 AR198595	AR198595 Sequence
33	421.2	98.9	699	6 AX050399	AX050399 Sequence
34	421.2	98.9	815	6 AX234496	AX234496 Sequence
35	421.2	98.9	815	9 S85192	S85192 Homo sapien
36	420.4	98.7	576	6 A64392	A64392 Sequence 5
37	420.4	98.7	576	6 AR198593	AR198593 Sequence
38	420.4	98.7	576	6 AX050395	AX050395 Sequence
39	420.4	98.7	640	9 AY047581	AY047581 Homo sapi
40	420.4	98.7	990	6 AX039419	AX039419 Sequence
41	420.4	98.7	990	6 AX135799	AX135799 Sequence
42	420.4	98.7	990	6 AX234351	AX234351 Sequence
43	420.4	98.7	990	6 AX409689	AX409689 Sequence
44	420.4	98.7	990	6 BD006221	BD006221 Variants
45	420.4	98.7	990	9 H066GFAA	M32977 Human hepar

ALIGNMENTS

RESULT 1  
HSA010438  
LOCUS  
DEFINITION Homo sapiens mRNA for vascular endothelial growth factor, splicing variant VEGF183.  
ACCESSION AJ010438  
VERSION AJ010438.1 GI:3647280  
KEYWORDS vascular endothelial growth factor; vegf gene; VEGF183 protein.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
AUTHORS Pei,D.  
TITLE Direct Submission















— 2 —



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RESULT 7
US-09-795-006A-146
; Sequence 146, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Allitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(767)
US-09-795-006A-146

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	Query Match	98.7%	Score 420.4;	DB 10;	Length 480;
	Best Local Similarity	99.8%;	Pred. No. 8.4e-120;		
	Matches 421; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATGAACTTTCGCTGTCTTGGGTGCATTGGAGCCTTGCTTGCTGCTCTACCTCCACCAT	60		
Db	57	ATGAACTTTCGCTGTCTTGGGTGCATTGGAGCCTTGCTTGCTGCTCTACCTCCACCAT	116		
Qy	61	GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAGGAGGCGCAGCATCATCAGCAAGTG	120		
Db	117	GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAGGAGGCGCAGCATCATCAGCAAGTG	176		





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; LENGTH: 388
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
; NAME/KEY: CDS
; LOCATION: (8)..(385)
US-09-795-006A-42

Query Match          63.8%; Score 271.8; DB 10; Length 388;
Best Local Similarity 90.1%; Pred. No. 3.6e-74;
Matches 291; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 100 GGGCAGAAATCATCAGCAAGTGGTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCAT 159
Db 8 GGGCAGAAATCATCAGCAAGTGGTGAATTCATGGATGCTATCAGCGCAGCTACTGCCAT 67

QY 160 CCAATCGAGACCTCGTGGACATCTCCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219
Db 68 CCGATCGAGACACTGGTGGACATCTCCAGGAAATTTGGAGTCCGACAAACACCTTCTTC 127

QY 220 AAGCCATCTGTGTCGCCCTGATGCGATCGCGGGCTGCTGCAATCAGCAGGCGCTGGAG 279
Db 128 AAGCCACCATGTGTGTCGCTGTACAGATGTGGGGTGTGCTGCAATGACGAAGGCTGGAG 187

QY 280 TGTGTGCCCACTGAGGAGTCCAAACATCACCATGCGAGATTATCGGATCAAACTCACCAC 339
Db 188 TCGTGTCCCAAGGAGTCCAAACATCACCATGCGAGATTATGAGAATTAACCTCACCAC 247

QY 340 GGCCAGCAGATAGGAGATGAGCTTCTTACAGCACAACAAATGTGAATGCGAGACCAAG 399
Db 248 GGCCAGCAGATCGGAGATGAGCTTCTTCCAGCATAACAAATGTGAATGTAGACCAAG 307

QY 400 AAAGATAGCAAGCAAGAAA 422
Db 308 AAAGATTGGTTCGAACAAAA 330

RESULT 14
US-09-795-006A-50
; Sequence 50, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA
; NAME/KEY: CDS
; LOCATION: (8)..(322)
US-09-795-006A-50

Query Match          55.7%; Score 237.2; DB 10; Length 322;
Best Local Similarity 85.9%; Pred. No. 1.4e-63;
Matches 263; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 100 GGGCAGAAATCATCAGCAAGTGGTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCAT 159
Db 8 GGGCAGAAATCATCAGCAAGTGGTGAATTCATGGATGCTATCAGCGCAGCTACTGCCAT 67
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QY 160 CCAATCGAGACCTCGTGGACATCTCCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219
Db 68 CCGATCGAGACACTGGTGGACATCTCCAGGAAATTTGGAGTCCGACAAACACCTTCTTC 127

QY 220 AAGCCATCTGTGTCGCCCTGATGCGATCGCGGGCTGCTGCAATCAGCAGGCGCTGGAG 279
Db 128 AAGCCACCATGTGTGTCGCTGTACAGATGTGGGGTGTGCTGCAATGACGAAGGCTGGAG 187

QY 280 TGTGTGCCCACTGAGGAGTCCAAACATCACCATGCGAGATTATCGGATCAAACTCACCAC 339
Db 188 TCGTGTCCCAAGGAGTCCAAACATCACCATGCGAGATTATGAGAATTAACCTCACCAC 247

QY 340 GGCCAGCAGATAGGAGATGAGCTTCTTACAGCACAACAAATGTGAATGCGAGACCAAG 399
Db 248 GGCCAGCAGATCGGAGATGAGCTTCTTCCAGCATAACAAATGTGAATGTAGACCAAG 307

QY 400 AAAGAT 405
Db 308 AAAGAT 313

RESULT 15
US-09-795-006A-54
; Sequence 54, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
; NAME/KEY: CDS
; LOCATION: (8)..(385)
US-09-795-006A-54

Query Match          54.8%; Score 233.4; DB 10; Length 388;
Best Local Similarity 82.7%; Pred. No. 2.3e-62;
Matches 267; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 100 GGGCAGAAATCATCAGCAAGTGGTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCAT 159
Db 8 GGGCAGAAATCATCAGCAAGTGGTGAATTCATGGATGCTATCAGCGCAGCTACTGCCAT 67

QY 160 CCAATCGAGACCTCGTGGACATCTCCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219
Db 68 CCGATCGAGACACTGGTGGACATCTCCAGGAAATTTGGAGTCCGACAAACACCTTCTTC 127

QY 220 AAGCCATCTGTGTCGCCCTGATGCGATCGCGGGCTGCTGCAATCAGCAGGCGCTGGAG 279
Db 128 AAGCCACCATGTGTGTCGCTGTACAGATGTGGGGTGTGCTGCAATGACGAAGGCTGGAG 187

QY 280 TGTGTGCCCACTGAGGAGTCCAAACATCACCATGCGAGATTATCGGATCAAACTCACCAC 339
Db 188 TCGTGTCCCAAGGAGTCCAAACATCACCATGCGAGATTATGAGAATTAACCTCACCAC 247

QY 340 GGCCAGCAGATAGGAGATGAGCTTCTTACAGCACAACAAATGTGAATGCGAGACCAAG 399
Db 248 GGCCAGCAGATCGGAGATGAGCTTCTTCCAGCATAACAAATGTGAATGTAGACCAAG 307

QY 400 AAAGATAGCAAGCAAGAAA 422
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Db 308 AAAGATTGGCTCTCGAACAAA 330  
||||| | ||||

Search completed: November 20, 2002, 03:30:41  
Job time : 248 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 20, 2002, 02:38:02 ; Search time 2195 Seconds  
(without alignments)  
3143.179 Million cell updates/sec

Title: US-09-884-050-1

Perfect score: 426

Sequence: 1 atgaactttctgtcttctg.....gagcaagacagaagtaa 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	94.4	528	14	BQ674897
c 2	388.4	91.2	459	9	AI591060
c 3	325.2	76.3	752	14	BQ780197
4	296	69.5	890	13	BI869727
5	270	63.4	600	12	BG803325
6	226.6	53.2	719	12	BG864739

c 7	204.4	48.0	534	14	BM991154
8	203.2	47.7	649	12	BF679862
9	193.8	45.5	208	10	BE166230
10	185.8	43.6	600	12	BG802357
11	147.4	34.6	540	9	AA308077
12	145.4	34.1	953	14	BQ713895
c 13	139.4	32.7	618	13	BI295068
14	119.4	28.0	413	14	BM756993
15	119.4	28.0	507	14	BM757090
16	119.4	28.0	522	14	BM751763
17	119.4	28.0	582	14	BM757101
18	119.4	28.0	636	14	BM742573
19	119.4	28.0	195	9	AU052024
20	119	27.9	127	13	BI771285
21	119	27.9	963	14	BQ893335
22	118.6	27.8	455	9	AI272466
23	118.6	27.8	997	9	AL530856
24	118.4	27.8	489	13	BI790853
25	118.4	27.8	829	10	BE569697
26	118.4	27.8	933	14	BQ936933
27	118.4	27.8	936	13	BI905649
28	118	27.7	890	14	BQ644755
29	118	27.7	901	9	AL552106
30	118	27.7	903	9	AL546005
31	118	27.7	925	9	AL547463
32	118	27.7	1023	9	AL543185
33	118	27.7	1031	14	BQ070531
34	117.6	27.6	869	9	AL552344
35	117.6	27.6	963	9	AL540600
36	117.4	27.6	759	13	BI685632
37	117.2	27.5	792	9	AL545800
38	117.2	27.5	887	14	BQ881520
39	117	27.5	1073	14	BQ070196
40	116.8	27.4	744	13	BI663772
41	116.8	27.4	900	14	BQ647895
42	116.4	27.3	488	14	HI11172
43	116	27.2	590	13	BI345094
44	115.6	27.1	913	9	AL553367
45	115.4	27.1	498	14	RI9956

#### ALIGNMENTS

RESULT 1  
BQ674897  
LOCUS BQ674897  
DEFINITION AGENCOURT\_8036450 NIH\_MGC\_102 Homo sapiens cdna clone IMAGE:6212223  
5', mRNA sequence.  
ACCESSION BQ674897  
VERSION BQ674897.1 GI:21785731  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 528)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM2375 row: p column: 16  
High quality sequence stop: 527.  
Location/Qualifiers 1..528





ACCESSION BQ780197  
 VERSION BQ780197.1 GI:21988669  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 752)  
 REFERENCE Bernaldo, M.F., Lennon, G. and Soares, M.B.  
 AUTHORS Normalization and subtraction: two approaches to facilitate gene  
 TITLE discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Jeff Stevens  
 CDNA Library prepared by: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: DISTRIBUTION: Researchers may obtain clones  
 from Research Genetics (www.resgen.com).  
 The following repetitive elements were found in this CDNA  
 sequence: 1-39, >POLY(A)Simple\_repeat (matched complement) 546-578;  
 >GC-richLow\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 Source Location/Qualifiers  
 1..752  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-PF0-cpb-1-06-0-UI"  
 /clone\_lib="UI-R-PF0"  
 /tissue\_type="Mixed tissues"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Vector: pT73-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-R-PF0 is a  
 subtracted CDNA library containing the following tissue(s)  
 ): Normal cartilage and SR-JWS Tumor Line . The  
 subtraction was made according to Bernaldo, Lennon and  
 Soares, Genome Research, 6:791-806, 1996. The  
 oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dtt)18 tail. The  
 sequence tags for these libraries are: CTAATGGACG,  
 CATTCTTGTA.  
 TAG\_LIB=UI-R-PF0  
 TAG\_TISSUE=cartilage  
 TAG\_SEQ=CTAATGGACG"

BASE COUNT 109 a 246 c 205 g 189 t 3 others  
 ORIGIN  
 Query Match 76.3%; Score 325.2; DB 14; Length 752;  
 Best Local Similarity 86.9%; Pred. No. 4.9e-70;  
 Matches 370; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 ATGAACCTTTCTGCTGTTGGGTGCATGGAGCCTTGCTGCTCTACCTCCACCAT 60  
 |||||||  
 DB 431 ATGAACCTTTCTGCTGTTGGGTGCATGGAGCCTTGCTGCTCTACCTCCACCAT 372  
 |||||||  
 QY 61 GCGAAGTGTGCCAGGCTGCACCCATGGCAGAGAGGAGGCGAGCAATCATCAGCAAGTG 120  
 |||||||  
 DB 371 GCCAAGTGTGCCAGGCTGCACCCACGACAGAGAGGAGGAGCAATCATCAGCAAGTG 315  
 |||||||  
 QY 121 GTGAAGTGTGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCGTGGTGAC 180  
 |||||||  
 DB 314 GTGAAGTGTGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCGTGGTGAC 255

QY 181 ATCTTCCAGGAGTACCTGTAGATCGAGTACATCTTCAAGCCATCTCTGTGCCCTG 240  
 |||||||  
 DB 254 ATCTTCCAGGAGTACCTGTAGATCGAGTACATCTTCAAGCCGCTCTGTGCCCTA 195  
 |||||||  
 QY 241 ATGCGATGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 300  
 |||||||  
 DB 194 ATGCGGTGTGCGGGCTGCTGCAATGATGAAGCCCTGGAGTGTGCGCCAGCTCGGAGC 135  
 |||||||  
 QY 301 ACATCACCATGACAGATTTATGCGGATCAACCTCACCAGGCCAGCACATAGGAGAGATG 360  
 |||||||  
 DB 134 AAGTCACTATGAGATCATGCGGATCAACCTCACCAGGCCAGCACATAGGAGAGATG 75  
 |||||||  
 QY 361 AGCTTCTTACAGCACACAATAATGTAATGCAGACCAAGAAAGATAGACGAACAAGAA 420  
 |||||||  
 DB 74 AGCTTCTTACAGCACACAATAATGTAATGCAGACCAAGAAAGATAGACGAACAAGAA 15  
 |||||||  
 QY 421 AAGTAA 426  
 || ||  
 DB 14 AAAAAA 9

RESULT 4  
 BI869727  
 LOCUS 603393614F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5403771 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI869727  
 VERSION BI869727.1 GI:16043400  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 890)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12029 row: k column: 04  
 High quality sequence stop: 733.

FEATURES  
 Source Location/Qualifiers  
 1..890  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5403771"  
 /clone\_lib="NIH\_MGC\_90"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: liver; Vector: PCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 Kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

BASE COUNT 246 a 246 c 256 g 142 t  
 ORIGIN  
 Query Match 69.5%; Score 296; DB 13; Length 890;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-63;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TTCATGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGACATCTTC 186  
 |||||||  
 DB 1 TTCATGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGACATCTTC 60

```

QY 187 CAGAGTACCTGATGAGATCGAGTACATCTCAAGCCATCCTGTGTGCCCCCTGATGCGA 246
|||||
Db 61 CAGAGTACCTGATGAGATCGAGTACATCTCAAGCCATCCTGTGTGCCCCCTGATGCGA 120
|||||
QY 247 TGGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCCCACTGAGGAGTCCACATC 306
|||||
Db 121 TGGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCCCACTGAGGAGTCCACATC 180
|||||
QY 307 ACCATGAGATTTATGCGGATCAAACTCCAAAGGCCAGCACATAGAGAGATGAGCTTC 366
|||||
Db 181 ACCATGAGATTTATGCGGATCAAACTCCAAAGGCCAGCACATAGAGAGATGAGCTTC 240
|||||
QY 367 CTACAGCACAAATGTGAATGACAGACCAAGAAAGAGATAGACAGACAGAAA 422
|||||
Db 241 CTACAGCACAAATGTGAATGACAGACCAAGAAAGAGATAGACAGACAGAAA 296
|||||

RESULT 5
BG803325 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0223-76 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803325
VERSION BG803325.1 GI:17950226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
AUTHORS Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
MEDLINE 21671825
COMMENT Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES
Source
1..600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dt. RNA Isolation: cytoplasmic RNA preps
(Manniatils); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCTCAATGTCGAGTGTGTGCCCACTGAGTGTGTGCCCACTGAGGAGTCCACATC
Information regarding entire library may be found at
http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies.htm."

BASE COUNT 131 a 183 c 196 g 90 t
ORIGIN

Query Match 63.4%; Score 270; DB 12; Length 600;
Best Local Similarity 86.6%; Pred. No. 2e-56;
Matches 310; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 ATGAACCTTTCTGCTGCTTGGGTGCAATGGAGCTTGGCTGCTGCTTACCTCCACCAT 60
|||||
Db 246 ATGAACCTTTCTGCTGCTTGGGTGCAATGGAGCTTGGCTGCTGCTTACCTCCACCAT 305
|||||
QY 61 GCCAAGTGTGCCAGGCTGCACCCATCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
|||||
Db 306 GCCAAGTGTGCCAGGCTGCACCCACGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 362
|||||
QY 121 GTGAAGTTCATGATGCTTATCAGCCGACGACTACTGCCATCCATCAGAGACCCCTGGTGGAC 180
|||||

```

```

Db 363 ATCAAGTTTCATGATGTCTACCGAGCAAGCTACTGCGCTCCGATTGAGACCCCTGGTGGAC 422
|||||
QY 181 ATCTTCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240
|||||
Db 423 ATCTTCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCTGTGTGCCCTG 482
|||||
QY 241 ATCGATGCGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCCCACTGAGGAGTCC 300
|||||
Db 483 ATCGCTGTGCAAGCTGCTTAACGATGAAGCCCTGGAGTGCCTGCCACGTCAGAGAGC 542
|||||
QY 301 AACATCACCATGAGATTTATGCGGATCAAACTCCAAAGGCCAGCACATAGAGAGAGA 358
|||||
Db 543 AACATCACCATGAGATTCATGCGGATCAAACTCCAAAGGCCAGCACATAGAGAGAGA 600
|||||

RESULT 6
BG864739 719 bp mRNA linear EST 29-MAY-2001
LOCUS 602799154F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4934916 5',
DEFINITION mRNA sequence.
ACCESSION BG864739
VERSION BG864739.1 GI:14215277
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10864 row: k column: 13
High quality sequence stop: 715.

FEATURES
Source
1..719
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4934916"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996).".

BASE COUNT 156 a 205 c 245 g 113 t
ORIGIN

Query Match 53.2%; Score 226.6; DB 12; Length 719;
Best Local Similarity 85.0%; Pred. No. 1.1e-45;
Matches 266; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 ATGAACCTTTCTGCTGCTTGGGTGCAATGGAGCTTGGCTGCTGCTTACCTCCACCAT 60
|||||
Db 312 ATGAACCTTTCTGCTGCTTGGGTGCAATGGAGCTTGGCTGCTGCTTACCTCCACCAT 371
|||||
QY 61 GCCAAGTGTGCCAGGCTGCACCCATGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
|||||

```



```

FEATURES
  source
    high quality sequence stop: 206.
    Location/Qualifiers
      1..208
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="HT0489"
        /dev_stage="Adult"
        /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
        Site_2: SmaI; A mini-library was made by cloning products
        derived from ORESPEC PCR (U.S. Letters Patent application
        NO. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
        BASE COUNT      51 a      57 c      56 g      44 t
        ORIGIN
          Query Match      45.5%; Score 193.8; DB 10; Length 208;
          Best Local Similarity 99.0%; Pred. No. 1.1e-37;
          Matches 195; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

FEATURES
source
fax: 713 790 0329.
Location/Qualifiers
1. .600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14 5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/notes="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
(Wanniatlis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCACCTGAATCTGAGTG--->. Other
information regarding entire library may be found at
http://pba.swmed.edu/bata/Libraries/microarray_cdna_librar
ies.htm."
121 a 180 c 210 g 89 t
BASE COUNT
ORIGIN

```

```

Query Match      43.6%; Score 185.8; DB 12; Length 600;
Best Local Similarity 87.8%; Pred. No. 1.2e-35;
Matches 215; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGAAC TTCTGCTG TCTTGG GTGCAT TGGAG CCTTG CCTTGT GCTTAC CTTCC ACCAT 60
    |||||
Db 359 ATGAAC TTCTGCTC TCTTGG GTGCA CTGGAC CCTTG GCTTTA CTGCTG TACCTC CACCAT 418
    |||||

QY 61 GCCAAG TGGTCC AGGCTG CACCCAT GGCAGA AGAGAG GGGCAGA ATCATC ACGAAG TG 120
    |||||
Db 419 GCCAAG TGGTCC AGGCTG CACCCAG CAGAGA ---AGG AGAGC AGAAGT GCCCAT GTAAGT G 475
    |||||

```





```
/clone="S6SNU620-22-C03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
```

```
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

```
BASE COUNT      131 a  108 c  108 g  66 t
ORIGIN
```

```
Query Match      28.0%; Score 119.4; DB 14; Length 413;
Best Local Similarity 99.2%; Pred. No. 2.9e-19;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 304 ATCACCATGCAGATTATGGGGATCAAACTCACCAAGGCCAGCACATAGGAGATGAGC 363
|||||
```

```
Db 1 ATCACCATGCAGATTATGGGGATCAAACTCACCAAGGCCAGCACATAGGAGATGAGC 60
|||||
```

```
QY 364 TTCCTACAGCAACAACAAATGTGAATGCAGACCAACCAAGAGATAGACCAAGAAAG 423
|||||
```

```
Db 61 TTCCTACAGCAACAACAAATGTGAATGCAGACCAACCAAGAGATAGACCAAGAAAG 120
|||||
```

```
QY 424 T 424
|
```

```
Db 121 T 121
```

## RESULT 15

BM757090

LOCUS K-EST0035851 S6SNU620 Homo sapiens cDNA clone S6SNU620-21-D03 5',

DEFINITION 507 bp mRNA linear EST 04-MAR-2002

RNA sequence.

ACCESSION BM757090

VERSION BM757090.1 GI:19086705

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 507)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel.: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 21 row: D column: 03

High quality sequence stop: 507.

FEATURES Location/Qualifiers

1..507

/organism="Homo sapiens"

```
/db_xref="taxon:9606"
/clone="S6SNU620-21-D03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
```

```
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

```
/lab_host="Top10F"
BASE COUNT      158 a  131 c  124 g  94 t
ORIGIN
```

```
Query Match      28.0%; Score 119.4; DB 14; Length 507;
Best Local Similarity 99.2%; Pred. No. 3e-19;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 304 ATCACCATGCAGATTATGGGGATCAAACTCACCAAGGCCAGCACATAGGAGATGAGC 363
|||||
```

```
Db 1 ATCACCATGCAGATTATGGGGATCAAACTCACCAAGGCCAGCACATAGGAGATGAGC 60
|||||
```

```
QY 364 TTCCTACAGCAACAACAAATGTGAATGCAGACCAACCAAGAGATAGACCAAGAAAG 423
|||||
```

```
Db 61 TTCCTACAGCAACAACAAATGTGAATGCAGACCAACCAAGAGATAGACCAAGAAAG 120
|||||
```

```
QY 424 T 424
|
```

```
Db 121 T 121
```

Search completed: November 20, 2002, 04:53:37

Job time : 2225 secs

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OM protein - protein search, using sw model

Run on: November 20, 2002, 03:27:51 ; Search time 73 seconds  
(without alignments)  
257.374 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLQHNKCEPRKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	147	16 AAR91075	Human vascular end
2	792	100.0	147	17 AAR94001	VEGF121. Homo sap
3	792	100.0	147	19 AAW62524	Amino acid sequenc
4	792	100.0	147	21 AAY90402	VEGF encoded by cl
5	792	100.0	147	21 AAY69412	Amino acid sequenc
6	792	100.0	147	21 AAY83033	Human vascular end
7	792	100.0	147	22 AAB98080	Human VEGF splice
8	792	100.0	147	22 AAB50427	Human vascular end
9	792	100.0	147	22 AAB50431	Human VEGF121. Ho
10	792	100.0	147	23 ABB76299	Human vascular end

11	792	100.0	164	20 AAY43482	Amino acid sequenc
12	792	100.0	171	20 AAY07473	Human VEGF(145) pr
13	792	100.0	188	20 AAY43484	Amino acid sequenc
14	792	100.0	191	19 AAW62525	Amino acid sequenc
15	792	100.0	208	20 AAY43483	Amino acid sequenc
16	792	100.0	213	21 AAY83036	Human vascular end
17	792	100.0	213	22 AAB50434	Human VEGF189. Ho
18	792	100.0	213	23 ABB76302	Human vascular end
19	792	100.0	215	11 AAR05102	Human vascular per
20	792	100.0	215	16 AAR91077	Human vascular end
21	792	100.0	215	17 AAR94003	VEGF189. Homo sap
22	792	100.0	215	19 AAB62526	Amino acid sequenc
23	792	100.0	215	21 AAB10645	Human VEGF protein
24	792	100.0	215	21 AAY90404	VEGF encoded by cl
25	792	100.0	215	21 AAY69415	Amino acid sequenc
26	792	100.0	215	21 AAY94803	Human VEGF. Homo
27	792	100.0	215	21 AAY57035	Human A215 amino a
28	792	100.0	215	22 AAB37512	Human VEGF C subun
29	792	100.0	232	16 AAR91078	Human vascular end
30	792	100.0	232	17 AAR94004	VEGF206. Homo sap
31	792	100.0	232	19 AAW62527	Amino acid sequenc
32	792	100.0	232	20 AAY43481	Amino acid sequenc
33	792	100.0	232	21 AAY90405	VEGF encoded by cl
34	792	100.0	232	21 AAY69416	Amino acid sequenc
35	792	100.0	232	21 AAY83037	Human vascular end
36	792	100.0	232	22 AAU08464	Polypeptide for hu
37	792	100.0	232	22 AAB50435	Human VEGF206. Ho
38	792	100.0	232	23 ABB76303	Human vascular end
39	792	100.0	398	20 AAY29418	Human vascular end
40	787	99.4	174	22 AAB82531	Vascular endotheli
41	787	99.4	191	11 AAR08002	Human vascular end
42	787	99.4	191	16 AAR91076	Human vascular end
43	787	99.4	191	17 AAW00724	Vascular endotheli
44	787	99.4	191	17 AAR94002	VEGF165. Homo sap
45	787	99.4	191	19 AAB93331	Human VEGF protein

ALIGNMENTS

RESULT 1

AAR91075

ID AAR91075 standard; Protein; 147 AA.

XX AAR91075;

AC AAR91075;

XX 14-MAY-1996 (first entry)

DT Human vascular endothelial growth factor-121, VEGF-121.

DE Conjugate; growth factor; FGF; cytotoxin; saporin; eye; regulation;  
KW cell proliferation; psoriasis; pterygia; corneal clouding; cancer;  
KW rheumatoid arthritis; vascular endothelial; fibroblast; epidermal;  
KW heparin binding.  
KW Homo sapiens.  
OS Homo sapiens.  
PH Key Location/Qualifiers  
FT Peptide 1..26  
FT Protein /label= sig\_peptide  
FT 27..147  
FT /label= VEGF-121

XX WO9524928-A2.

PN 21-SEP-1995.

XX 15-MAR-1995; 95WO-US03448.

XX 15-MAR-1994; 94US-0213447.

PR 15-MAR-1994; 94US-0213446.

XX (PRIZ-) PRIZM PHARM INC.

XX PI Baird JA, Houston LL, Nova MP, Sosnowski BA;  
 XX WPI; 1995-336820/43.  
 XX DR N-PSDB; AAQ99080.  
 XX PI New conjugates of growth factor receptor ligand and targetted agent  
 PT - partic. DNA or cytotoxin, used to control cell proliferation in  
 PT the eye, e.g. to prevent growth of pterygii and corneal clouding  
 XX  
 XX PS Disclosure; Page 184-185; 204pp; English.  
 XX  
 CC AAR91075-R91078 are human vascular endothelial growth factors (VEGFs).  
 CC DNA encoding a VEGF can be used to create a fusion protein (FP),  
 CC the cDNA of which includes a nucleic acid binding domain (NABD) and  
 CC encodes a heparin binding growth factor, HEPGF (e.g. VEGF, HBEGF),  
 CC a protein synthesis inhibitor and opt. a linker imparting flexibility  
 CC to the FP. The FP can be used to target a protein synthesis inhibitor,  
 CC an antisense DNA sequence or an inhibitor of elongation factor 2, to a  
 CC cell carrying a HEPGF receptor. The conjugates of the invention are  
 CC used to inhibit cell proliferation in cells carrying the particular  
 CC growth factor receptor. A specific application is to prevent  
 CC excessive proliferation of epithelial cells, fibroblasts and  
 CC keratinocytes in the anterior eye after surgery, partic. to prevent  
 CC recurrence of pterygii after surgical removal, closure of  
 CC trabeculectomy after glaucoma surgery and corneal clouding after  
 CC eximer laser treatment. Other conditions which may be treated include  
 CC tumours, restenosis, psoriasis, Dupuytren's contracture, diabetic  
 CC complications, Kaposi's sarcoma and rheumatoid arthritis.  
 XX  
 XX SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 16; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWVHWSALLLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWVHWSALLLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKDRARQEK 141  
 Db 121 SFLQHNKCECRPKDRARQEK 141  
 RESULT 2  
 AAR94001  
 ID AAR94001 standard; Protein; 147 AA.  
 XX  
 XX AC AAR94001;  
 XX  
 XX DT 09-OCT-1996 (first entry)  
 XX  
 XX DE VEGF121.  
 XX  
 KW Vascular endothelial growth factor; VEGF; human; conjugate; tumour; iris;  
 KW proliferation inhibition; VEGF-mediated pathophysiological condition;  
 KW dermatological disorder; VEGF receptor; vascular proliferation; retina;  
 KW ophthalmic disorder; hyperproliferating blood vessel; therapy; psoriasis;  
 KW conjunctiva; vitreous humour; rheumatoid arthritis; skin cancer;  
 KW varicose veins; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX WO9606641-A1.  
 XX  
 XX PD 07-MAR-1996.  
 XX  
 XX PF 29-AUG-1995; 95WO-US10973.

XX PR 16-MAY-1995; 95US-0441979.  
 XX PR 29-AUG-1994; 94US-0297961.  
 XX PA (PRIZ-) PRIZM PHARM INC.  
 XX PI Fleurbaaij GA, Freund E, Houston LL, Nova MP, Sosnowski BA;  
 PI Victor KD;  
 XX WPI; 1996-160151/16.  
 XX DR N-PSDB; AAT17613.  
 XX  
 PT Vascular endothelial cell growth factor (VEGF) conjugates - having  
 PT VEGF linked to targeted agent, used for inhibiting proliferation of  
 PT cells, e.g. for gene therapy  
 XX  
 PS Disclosure; Page 122-123; 193pp; English.  
 XX  
 CC AAR94001-R94004, AAR94031, AAR94032, AAR94039 and AAR94040 represent  
 CC vascular endothelial growth factors (VEGF). This sequence represents  
 CC VEGF121. These sequences were used in VEGF conjugates of the invention.  
 CC In the conjugates, VEGF (or fragments of it) are linked to a targeted  
 CC agent (this can be via a linker sequence), so that the conjugate binds to  
 CC a VEGF receptor. Cys-modified forms of VEGF are particularly suitable  
 CC for chemical conjugation to linkers and targeted agents. The conjugates  
 CC are used for inhibiting proliferation of cells bearing VEGF receptors.  
 CC They can be used for treating a VEGF-mediated pathophysiological  
 CC condition, including dermatological disorders with underlying vascular  
 CC proliferation, solid tumours or an ophthalmic disorder of  
 CC hyperproliferating blood vessels of the retina, iris, conjunctiva or  
 CC vitreous humour. The conjugates can also be used for treating  
 CC psoriasis, rheumatoid arthritis, skin cancers and other tumours, or  
 CC varicose veins. They are also suitable for use in gene therapy.  
 XX  
 XX SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 17; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWVHWSALLLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWVHWSALLLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKDRARQEK 141  
 Db 121 SFLQHNKCECRPKDRARQEK 141  
 RESULT 3  
 AAW62524  
 ID AAW62524 standard; Protein; 147 AA.  
 XX  
 XX AC AAW62524;  
 XX  
 XX DT 11-SEP-1998 (first entry)  
 XX  
 DE Amino acid sequence of human VEGF-121.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF; production;  
 KW nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;  
 KW blood vessel; essential hypertension; pulmonary arterial hypertension;  
 KW PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;  
 KW coronary bypass operation; anastomosis; endarterectomy.  
 XX  
 OS Homo sapiens.  
 XX WO9820027-A2.  
 XX  
 XX PN

```

PD 14-MAY-1998.
XX
PF 03-NOV-1997; 97WO-GB03015.
XX
PR 21-AUG-1997; 97GB-0017791.
XX
PR 01-NOV-1996; 96GB-0022852.
XX
PR 09-MAY-1997; 97GB-0009494.
XX
FA (EURO-) EUROGENE LTD.
XX
XX Barker SGE, Martin JF, Yla-Herttuala S;
PI WPI; 1998-286857/25.
XX
DR N-PSDB; AAV38450.
XX
XX Treatment of prevention of intimal hyperplasia by stimulating
PT production of nitric oxide - by administration of vascular
PT endothelial growth factor, useful for, e.g. treating or preventing
PT intimal hyperplasia
XX
XX Claim 8; Page 54; 70pp; English.
XX
XX The present sequence represents human vascular endothelial growth factor
CC 121 (VEGF-121). VEGF stimulates production of nitric oxide and
CC prostacyclin. VEGF can therefore be used for treatment or prevention
CC of intimal hyperplasia in a blood vessel. VEGF can be used for treating
CC or preventing any condition responsive to in vivo stimulation of
CC nitric acid and prostacyclin (especially essential hypertension,
CC pulmonary arterial hypertension (PAH), cor pulmonale and
CC atherosclerosis. VEGF is specifically used to control (re)stenosis,
CC where caused by PAH or by a surgical procedure such as angioplasty,
CC coronary bypass operation, anastomosis or endarterectomy.
XX
XX Sequence 147 AA;
XX
Query Match 100.0%; Score 792; DB 19; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNFLLSWVHSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Db 1 MNFLLSWVHSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Qy 61 IFQEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Db 61 IFQEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Qy 121 SFLQHNKCECRPKDRARQEK 141
Db 121 SFLQHNKCECRPKDRARQEK 141
XX
RESULT 4
AA90402
ID AA90402 standard; Protein; 147 AA.
XX
AC AA90402;
XX
XX 18-JUL-2000 (first entry)
XX
DE VEGF encoded by clone VEGF121, SEQ ID NO:1.
XX
KW Targetted gene delivery: fibroblast growth factor receptor;
KW FGFR-binding protein; nucleic acid binding protein;
KW receptor-internalised ligand; cytotoxin; saporin; gene therapy;
KW cytotide; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW rheumatoid arthritis; restenosis; Dupuytren's contracture; psoriasis;
KW eczema; heparin-binding epidermal growth factor; HBEGF;
KW vascular endothelial growth factor; VEGF.
XX
OS Unidentified.
XX
PN US6037329-A.

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XX 14-MAR-2000.
XX
XX 24-SEP-1996; 96US-0718904.
XX
XX 15-MAR-1994; 94US-0213446.
PR 15-MAR-1994; 94US-0213447.
PR 29-AUG-1994; 94US-0297961.
PR 13-SEP-1994; 94US-0305771.
PR 16-MAY-1995; 95US-0441979.
XX
XX (SELE-) SELECTIVE GENETICS INC.
XX
XX Chandler LA, Sosnowski BA, Baird JA;
PI WPI; 2000-292008/25.
XX
DR N-PSDB; AAA12853.
XX
XX Gene delivery system, useful for treating or preventing cancer and
PT rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT nucleic acid binding domain and nucleic acid
XX
XX Disclosure; Columns 83-84; 131pp; English.
XX
XX The invention relates to a novel gene delivery composition for the
CC targetted delivery of cytotoxins or prodrug-converting enzymes to
CC proliferating cells. The gene delivery composition comprises a protein
CC that binds the fibroblast growth factor receptor (FGFR) which is fused
CC or chemically conjugated to a nucleic acid binding domain. The nucleic
CC acid binding domain is complexed with a suitable expression construct
CC encoding a cytotoxin such as saporin. One or more linkers may join the
CC FGFR-binding protein to the nucleic acid binding protein. These are
CC selected to increase the specificity, toxicity, solubility, serum
CC stability or intracellular availability, and may serve to promote
CC condensation of nucleic acids for delivery to a cell. The fusion protein
CC binds to FGFR and is internalised by cells that carry this receptor. The
CC gene delivery composition is used for the therapeutic alteration of the
CC function, gene expression and viability of cells. In particular, it may
CC be used for the treatment and prevention of cell proliferative
CC disorders, for example after eye surgery, melanoma and many other sorts
CC of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC diabetic retinopathy, psoriasis and eczema. The gene delivery
CC compositions of the invention have high specificity for particular cells
CC and can deliver larger amounts of DNA compared to prior art methods.
CC Sequences AAA12853- AAA12856 represent cDNA clones encoding vascular
CC endothelial growth factor (VEGF), and sequences XAY90402-Y90405 represent
CC the encoded VEGF proteins. AAA12857 represents cDNA encoding human
CC heparin-binding epidermal growth factor (HBEGF) precursor, and
CC XAY90406-Y90409 represent HBEGF precursor and mature proteins.
XX
XX Sequence 147 AA;
XX
Query Match 100.0%; Score 792; DB 21; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNFLLSWVHSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Db 1 MNFLLSWVHSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Qy 61 IFQEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Db 61 IFQEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Qy 121 SFLQHNKCECRPKDRARQEK 141
Db 121 SFLQHNKCECRPKDRARQEK 141
XX
RESULT 5
AA9412
ID AAY69412 standard; Protein; 147 AA.
XX

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AC AAY69412;  
 DT 03-JUL-2000 (first entry)  
 DE Amino acid sequence of vascular endothelial growth factor 121.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF 121; angiogenic factor;  
 KW blood vessel injury; vascular injury; microvascular angiopathy;  
 KW thrombotic microangiopathy; kidney disease; haemolytic uremic syndrome;  
 KW toxic shock syndrome; venom; hypercoagulable state; platelet activation;  
 KW platelet aggregation; thrombosis; preclampsia; sepsis; pancreatitis;  
 KW intravascular coagulation; thrombotic thrombocytopenia purpura;  
 KW acute renal failure; myocardial infarction; ischemic bowel disease;  
 KW stroke; hypoxia; hypercapnia; fibrosis; toxic alveolar injury;  
 KW acute respiratory distress syndrome; pneumonia; pulmonary emboli;  
 KW birth prematurity disorder; wound; allergy; hypersensitivity;  
 KW autoimmune disease; organ transplant; focal glomerulosclerosis;  
 KW amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200013702-A2.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 09-SEP-1999; 99WO-US20480.  
 XX  
 PR 09-SEP-1998; 98US-0099694.  
 PR 26-MAR-1999; 99US-0126406.  
 PR 27-MAR-1999; 99US-0126615.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Schreiner GF, Johnson RJ;  
 XX  
 DR WPI: 2000-256861/22.  
 DR N-PSDB; AA299344.  
 XX  
 PT Novel methods and compositions for the prevention and treatment of  
 PT microvascular angiopathies by administration of angiogenic factors such  
 PT as vascular endothelial growth factor (VEGF)  
 XX  
 PS Disclosure; Fig 3; 46pp; English.  
 XX  
 CC The present sequence represents native human vascular endothelial growth  
 CC factor (VEGF) 121. VEGF is an angiogenic factor. VEGF proteins are used  
 CC for the prevention or repair of injury to blood vessels or associated  
 CC nonvascular tissues (served by the blood vessels) and for the prevention  
 CC and repair of vascular injury associated with microvascular angiopathy,  
 CC particularly thrombotic microangiopathy. The proteins methods may also  
 CC be used for the prevention and treatment of kidney diseases associated  
 CC with injury to, or atrophy of, the vasculature of the glomerulus and  
 CC interstitium. Conditions which may be treated include haemolytic uremic  
 CC syndrome, toxic shock syndrome, venom exposure, chemical exposure,  
 CC hypercoagulable states, platelet activation or aggregation, thrombosis,  
 CC preclampsia, thrombotic thrombocytopenia purpura, disseminated  
 CC intravascular coagulation, sepsis, pancreatitis, acute renal failure,  
 CC myocardial infarction, ischemic bowel disease, transient ischemic  
 CC attacks, stroke, hypoxia or hypercapnia or fibrosis arising from lung  
 CC endothelium injury, acute respiratory distress syndrome, toxic alveolar  
 CC injury, pneumonia, pulmonary emboli, birth prematurity disorders,  
 CC wounds, allergic reactions, hypersensitivity, autoimmune diseases, organ  
 CC transplants, focal glomerulosclerosis, and amyloidosis.  
 XX  
 SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 21; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWHNSALLLYLHAKWSQAAPNAEGGQNNHHEVVKFMDVYQSYCHPIETLYD 60  
 DB 1 MNFLSWHNSALLLYLHAKWSQAAPNAEGGQNNHHEVVKFMDVYQSYCHPIETLYD 60

QY 61 IFQEXPDEIEYIFKPSVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGHIGEM 120  
 DB 61 IFQEXPDEIEYIFKPSVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRAROEK 141  
 DB 121 SFLQHNKCECRPKKDRAROEK 141  
 RESULT 6  
 ID AAY83033 standard; Protein; 147 AA.  
 AC AAY83033;  
 XX  
 DT 04-JUL-2000 (first entry)  
 XX  
 DE Human vascular endothelial growth factor (hVEGF121).  
 XX  
 KW Vascular endothelial growth factor; human; angiogenesis; VEGF;  
 KW capillary formation; hypertension; treatment; kidney; CNS; stroke;  
 KW meningitis; central nervous system; tumour; infection; bone growth;  
 KW hypoxia; hypercapnia; fibrosis; inflammatory bowel disease;  
 KW diarrhoea; allografts; cardiac valve.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200013703-A2.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 09-SEP-1999; 99WO-US20481.  
 XX  
 PR 09-SEP-1998; 98US-0099694.  
 PR 26-MAR-1999; 99US-0126406.  
 PR 27-MAR-1999; 99US-0126615.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Schreiner GF, Johnson RJ;  
 XX  
 DR WPI: 2000-256862/22.  
 DR N-PSDB; AA293345.  
 XX  
 PT Novel methods for treating hypertension by administering a factor which  
 PT increases angiogenesis and/or vascular permeability  
 XX  
 PS Claim 5; Figure 6; 51pp; English.  
 CC Administering vascular endothelial growth factor (VEGF) can be used  
 CC for treating hypertension (especially salt-dependent hypertension)  
 CC Administration of VEGF promotes angiogenesis and/or vascular or  
 CC capillary permeability. The method is also useful in treating  
 CC disorders related to abnormal transport of solutes across endothelial  
 CC cells. Such disorders include the treatment or prevention of kidney  
 CC disease associated with impaired filtration or excretion of solutes;  
 CC the treatment or prevention of diseases of the central nervous system  
 CC associated with alterations in cerebrospinal fluid, e.g. stroke,  
 CC meningitis, tumour, infections, and bone growth disorders; treatment  
 CC or prevention of hypoxia or hypercapnia or fibrosis arising from  
 CC accumulation of fluid secretions in the lungs, e.g. acute respiratory  
 CC distress syndrome, toxic alveolar injury, pneumonia, infections,  
 CC surgical intervention, cystic fibrosis; treatment or prevention of  
 CC pulmonary dysfunction arising from injury to the pulmonary  
 CC endothelium, including disorders arising from premature birth, and  
 CC pulmonary hypertension; treatment or prevention of disease arising  
 CC from disordered transport of fluid and solutes across the intestinal  
 CC epithelium, e.g. inflammatory bowel disease, diarrhoea; treatment or  
 CC prevention of ascites accumulation in the peritoneum; enhancement of  
 CC efficacy of solute flux; preservation or enhancement of function of  
 CC organ allografts; and treatment of cardiac valve disease. This  
 CC sequence is the native human vascular endothelial growth

CC factor hVEGF121. The activity of VEGF is mediated by interaction  
 CC with specific receptors on target tissues, most notably the vascular  
 CC endothelium. VEGF exists as five different length monomer chains due  
 CC to alternative splicing of the VEGF RNA transcript. VEGF121 is  
 CC unique among the five forms in that it does not bind to heparin like  
 CC molecules associated with the extracellular matrix.

XX  
 SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 21; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Qy 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Qy 121 SFLQHNKCECRPKKDRARQEK 141  
 Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 7  
 AAB98080  
 ID AAB98080 standard; Protein; 147 AA.  
 XX  
 AC AAB98080;  
 XX  
 DT 16-AUG-2001 (first entry)  
 XX  
 DE Human VEGF splice variant VEGF121 protein SEQ ID NO:4.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF splice variant; VEGF;  
 KW VEGF121; colon cancer cell line acquired malignancy; anticancer.

XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= signal  
 FT Protein 27..147  
 FT /label= VEGF\_splice\_variant\_VEGF121  
 XX  
 PN JP2001061483-A.  
 XX  
 PD 13-MAR-2001.  
 XX  
 PF 31-AUG-1999; 95JP-0244198.  
 XX  
 PR 31-AUG-1999; 99JP-0244198.  
 XX  
 PA (EISA ) EISAI CO LTD.  
 XX  
 XX WPI; 2001-294711/31.  
 DR N-PSDB; AAH21876.  
 XX  
 PT Human colon cancer cell line is transfected with VEGF gene and selected  
 PT for having acquired malignancy -  
 XX  
 PS Example 1; Page 7; 8pp; Japanese.  
 XX  
 CC The present invention describes a method in which the vascular  
 CC endothelial growth cell (VEGF) gene is introduced to a human colon  
 CC cancer cell showing no malignancy, and a cell line highly expressing  
 CC VEGF is selected to get a cell line acquired malignancy. Also described  
 CC are: (1) a human colon cancer cell line acquired malignancy by the above  
 CC method; (2) WDR cell line acquired malignancy by the above method;  
 CC (3) a method for screening an anticancer agent by using the above human  
 CC colon cancer cell line, preferably WDR cell line, acquired malignancy;

CC and (4) a compound screened by the above method. The human colon cancer  
 CC cell line acquired malignancy can be used for screening an anticancer  
 CC agent. The present sequence represents the human VEGF splice variant  
 CC VEGF121, which is used in an example from the present invention.

XX  
 SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 22; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Qy 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Qy 121 SFLQHNKCECRPKKDRARQEK 141  
 Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 8  
 AAB50427  
 ID AAB50427 standard; Protein; 147 AA.  
 XX  
 AC AAB50427;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human vascular endothelial growth factor polypeptide.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF; VEGF dimer;  
 KW hypotensive; litholytic; nephrotropic; antiarteriosclerotic;  
 KW antiinflammatory; angiogenesis; vascular remodelling; injury; wound;  
 KW peripheral arterial disease; coronary artery disease; hypoxia;  
 KW essential hypertension; microvascular angiopathy; hypercapnia;  
 KW polycystic kidney disease; vascular endothelial cell repair;  
 KW lung disease; kidney disease; inflammatory bowel disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200071716-A2.  
 PN  
 XX 30-NOV-2000.  
 PD  
 XX 18-MAY-2000; 2000WO-US13636.  
 XX  
 PF 20-MAY-1999; 99US-0135312.  
 PR 20-JAN-2000; 2000US-0177407.  
 XX  
 XX (SCIO-) SCIOS INC.  
 PA  
 XX  
 PI Jue RA, Schellenberger U, Stathis PA, Adriaenssens PI, Abraham JA;  
 PI Baldwin PA, Pollitt NS;  
 XX  
 XX WPI; 2001-041064/05.  
 DR N-PSDB; AAC90473.  
 XX  
 PT Vascular endothelial growth factor dimer, useful for treating essential  
 PT hypertension, polycystic kidney diseases, microvascular angiopathy and  
 PT coronary artery disease, comprising two monomeric subunits -  
 XX  
 PS Example 1; Fig 1; 61pp; English.  
 XX  
 CC The present sequence encodes a monomer of a vascular endothelial growth  
 CC factor (VEGF) dimer. The dimer comprises a first and a second monomer,  
 CC each comprising at least amino acids 11-116 of a defined 147 amino acid  
 CC sequence, or a sequence having at least 90% identity to the defined  
 CC sequence, and retaining a cysteine at or corresponding to position 116,  
 CC which is disulphide-bonded to an additional extraneous cysteine. The

VEGF dimer is useful for inducing angiogenesis and vascular remodelling, treating peripheral arterial disease, coronary artery disease, essential hypertension, microvascular angiopathy and polycystic kidney disease, and repair of vascular endothelial cell layers. It is also useful for treating injuries, wounds, hypoxia, hypercapnia, pulmonary dysfunction, kidney diseases, diseases arising from disordered transport of solutes and fluids across the intestinal epithelium including inflammatory bowel disease, and disorders due to accumulation of ascites in the peritoneum.

Sequence 147 AA;  
Query Match 100.0%; Score 792; DB 22; Length 147;  
Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNFLSWVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
DB 1 MNFLSWVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120  
DB 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120  
QY 121 SFLOHNKCECRPKKDRARQEK 141  
DB 121 SFLOHNKCECRPKKDRARQEK 141

RESULT 9  
AAB50431  
ID AAB50431 standard; Protein; 147 AA.  
XX AAB50431;  
XX 13-MAR-2001 (first entry)  
DE Human VEGF121.  
XX Human; VEGF; vascular endothelial growth factor; VEGF121; VEGF145;  
KW cardiant; cerebroprotective; hypotensive; nephrotropic; antidiabetic;  
KW dermatological; immunosuppressive; antiinflammatory; cytostatic;  
KW vasotropic; antibacterial; angiogenesis; vascular remodelling;  
KW vascular disease; kidney disease; diabetes; systemic lupus erythematosus;  
KW meningitis; tumour; infection; lung disease inflammatory bowel disease.

Homo sapiens.  
XX WO200071713-A1.  
XX 30-NOV-2000.  
XX 18-MAY-2000; 2000WO-US13536.  
XX 20-MAY-1999; 99US-0135312.  
XX (SCIO-) SCIOS INC.  
XX Pollitt NS, Abraham JA;  
XX WPI; 2001-025162/03.  
XX N-PSDB; AAC90477.  
XX Enhancing biological activity of vascular endothelial growth factor by  
PT replacing a Cys residue, for producing variant useful for treating  
PT hypertension, stroke, diabetes, lupus, glomerulonephritis, meningitis,  
PT tumor, pneumonia, infections -  
XX Claim 5; Fig 3; 62pp; English.  
XX The present sequence is given in a specification relating to a method for  
CC enhancing the biological activity of a vascular endothelial growth factor  
CC (VEGF) originally having a cysteine residue at a position 116 of the 121

amino acid native mature human VEGF. The method comprises eliminating the cysteine residue to produce a VEGF variant. The variant is useful for inducing angiogenesis or vascular remodelling, for prevention or repair of injury to blood vessels, where injury is associated with haemolytic uraemic syndrome (HUS) or microvascular angiopathy such as thrombotic microangiopathy (TMA). The VEGF variant is also useful for treatment of essential hypertension in a patient. The variant is useful for treating coronary artery disease and/or peripheral arterial disease, to foster myocardial blood vessel growth and to improve blood flow to the heart. It is useful for the treatment and prevention of kidney diseases associated with injury to, or atrophy of, the vasculature of the glomerulus and interstitium and for the treatment and prevention of acute renal failure, myocardial infarction, ischaemic bowel disease, transient ischaemic attacks, stroke, hypoxia, hypercapnia, focal glomerulosclerosis, amyloidosis, glomerulonephritis, diabetes, systemic lupus erythematosus or chronic hypoxia/atrophy. It is also useful in the preservation or enhancement of function of organ allografts and xenografts, and for treating disorders related to abnormal transport of solutes across endothelial cells such as meningitis, tumour, infections, disorders of bone growth, acute respiratory distress syndrome, toxic alveolar injury, pneumonia, cystic fibrosis, inflammatory bowel disease, infectious diarrhoea or cardiac valve disease.

Sequence 147 AA;  
Query Match 100.0%; Score 792; DB 22; Length 147;  
Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNFLSWVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
DB 1 MNFLSWVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120  
DB 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120  
QY 121 SFLOHNKCECRPKKDRARQEK 141  
DB 121 SFLOHNKCECRPKKDRARQEK 141

RESULT 10  
ABB76299  
ID ABB76299 standard; Protein; 147 AA.  
XX ABB76299;  
XX 12-AUG-2002 (first entry)  
DE Human vascular endothelial growth factor 121.  
XX Vascular endothelial growth factor; VEGF; hVEGF121; human;  
KW hypertension; hypotensive; nephrotropic; cerebroprotective;  
KW antibacterial; cytostatic; antialcoholic; virucide; vasotropic;  
KW antidiarrhoeic; immunosuppressive; cardiant; antiinflammatory;  
KW angiogenic factor.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..26  
FT /label= Signal\_peptide  
FT 27..147  
FT /label= Mature\_protein  
XX US6352975-B1.  
XX 05-MAR-2002.  
XX 09-SEP-1999; 99US-0392932.  
XX 09-SEP-1998; 98US-099694P.

PR	26-MAR-1999;	99US-126406P.	
PR	27-MAR-1999;	99US-126615P.	
XX			
XX	(SCIO-) SCIOS INC.		
PA			
PI	Schreiner GF, Johnson RJ;		
PI			
DR	WPI; 2002-412951/44.		
DR	N-PSDB; ABL57427.		
XX			
PT	New method, useful in treatment of salt-sensitive hypertension,		
PT	comprises administration of a vascular endothelial growth factor to a		
PT	patient -		
XX			
PS	Claim 1; Fig 6; 30pp; English.		
XX			
CC	The present sequence is the protein sequence of human vascular		
CC	endothelial growth factor 121 (hVEGFl21), an isoform that is weakly		
CC	acidic and does not bind to heparin. The present invention		
CC	concerns methods for the treatment of salt-sensitive hypertension		
CC	by administering a VEGF in an amount effective to reduce the blood		
CC	pressure of a salt-sensitive hypertension patient to a normal range.		
CC	The VEGF is preferably hVEGFl21 or a VEGF having a heparin-binding		
CC	domain modified to render it incapable of binding heparin. The		
CC	VEGF may be co-administered with another angiogenic factor. The		
CC	method can also be used to treat disorders relating to abnormal		
CC	transport of solutes across endothelial cells, including treatment		
CC	or prevention of kidney disease associated with impaired filtration		
CC	or excretion of solutes, central nervous system diseases associated		
CC	with alterations in cerebrospinal fluid synthesis, composition or		
CC	circulation including stroke, meningitis, tumour, infections, and		
CC	disorders of bone growth, hypoxia or hypercapnia or fibrosis		
CC	arising from accumulation of fluid secretions in lungs or		
CC	impediments to their removal, including acute respiratory distress		
CC	syndrome, toxic alveolar injury as occurs in smoke inhalation,		
CC	pneumonia including viral and bacterial infections, surgical		
CC	interventions, cystic fibrosis, and other inherited or acquired		
CC	disease of the lung associated with fluid accumulation in the		
CC	pulmonary air space, pulmonary endothelium injury, disordered		
CC	transport of fluid and solutes across the intestinal epithelium,		
CC	including inflammatory bowel disease, infections, diarrhoea,		
CC	ascites accumulation in the peritoneum as occurs in the failure of		
CC	heart, liver and kidney, preservation and enhancement of function		
CC	of organ allografts, and cardiac valve disease.		
XX			
SQ	Sequence 147 AA;		
Query Match	100.0%;	Score 792;	DB 23; Length 147;
Best Local Similarity	100.0%;	Pred. No. 8.4e-76;	
Matches 141; Conservative	0;	Mismatches	0; Indels 0; Gaps
QY	1	MNFFLLSWHWSLALLYLHHAQWSAAPMAEGGQNHVVKFMDYVQRSYCHPIETFLVD	60
Db	1	MNFFLLSWHWSLALLYLHHAQWSAAPMAEGGQNHVVKFMDYVQRSYCHPIETFLVD	60
QY	61	IFOEYDPDEIYIFKPSVCLMRGCGCNDGEGLCVPTESNITMQIMRIKPHQGQHIGEM	120
Db	61	IFOEYDPDEIYIFKPSVCLMRGCGCNDGEGLCVPTESNITMQIMRIKPHQGQHIGEM	120
QY	121	SFTQHNKCECRPKDRARQEK	141
Db	121	SFTQHNKCECRPKDRARQEK	141
RESULT 11			
AAV43482			
ID	AAV43482 standard; Protein; 164 AA.		
XX			
AC	AAV43482;		
XX			
DT	26-JAN-2000 (first entry)		
XX			
DE	Amino acid sequence of VEGF-Al38 protein.		

DT 03-AUG-1999 (first entry)  
 XX Human VEGF(145) protein sequence.  
 DE  
 KW Human;vascular endothelial growth factor; VEGF; vector; stimulation;  
 KW angiogenesis; mammal; peripheral; cardiac; tissue; ischaemia; perfusion;  
 KW neovascularisation; muscle.  
 KW  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..26  
 FT /note= "signal peptide"  
 FT Protein 27..171  
 FT /note= "mature protein"  
 XX  
 XX WO9921590-A1.  
 XX  
 XX 06-MAY-1999.  
 XX  
 XX 23-OCT-1998; 98WO-US22668.  
 XX  
 XX 26-NOV-1997; 97GB-0024906.  
 XX  
 XX 27-OCT-1997; 97US-0063629.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Bett AJ, Huckle WR, Kendall RL, Thomas KA;  
 XX  
 XX WPI; 1999-302907/25.  
 XX  
 XX N-PSDB; AAX57724.  
 XX  
 XX Stimulating angiogenesis by expressing vascular endothelial growth  
 XX factor  
 XX  
 XX Example 1; Fig 2; 46pp; English.  
 XX  
 XX This sequence represents the 145 amino acid form of human vascular  
 CC endothelial growth factor (VEGF(145)). The coding sequence, when  
 CC administered in a vector, can be used to stimulate angiogenesis in a  
 CC mammal. Administration of the VEGF(145) is used to treat peripheral,  
 CC cardiac or other tissue ischaemias, i.e. to increase neovascularisation,  
 CC perfusion and performance of ischaemic muscle.  
 XX  
 XX Sequence 171 AA;  
 SQ  
 Query Match 100.0%; Score 792; DB 20; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 1e-75;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLLSVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLLSVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 DB 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 13  
 AAY43484  
 ID AAY43484 standard; Protein; 188 AA.  
 XX  
 XX AAY43484;  
 XX  
 XX 26-JAN-2000 (first entry)  
 DT  
 XX Amino acid sequence of VEGF-A162 protein.  
 DE  
 XX

KW Vascular endothelial factor; VEGF; VEGF-A162; variant; vascular disease;  
 KW cardiovascular disease; vascular cell proliferation; angioplasty;  
 KW restenosis; drug permeation; tumour; ischemic condition;  
 KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
 KW chronic lower limb ischemia; peripheral vascular disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..27  
 FT /note= "secretion signal sequence"  
 FT  
 XX WO9940197-A2.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 04-FEB-1999; 99WO-US02425.  
 XX  
 XX 06-FEB-1998; 98US-0073979.  
 XX  
 XX (COLL-) COLLATERAL THERAPEUTICS INC.  
 XX  
 XX Baird A, Andreason G;  
 XX  
 XX WPI; 1999-600967/51.  
 XX  
 XX N-PSDB; AAZ29998.  
 XX  
 XX New growth factor variants, useful for treating cardiovascular disease,  
 PT especially by stimulating vascular cell proliferation -  
 XX  
 XX Claim 9; Fig 5; 101pp; English.  
 XX  
 CC The present sequence represents vascular endothelial factor VEGF-A162.  
 CC It is a VEGF-A variant of the invention. The specification describes new  
 CC VEGF-A variants in which exon 6a is excluded (other forms which contain  
 CC both exon 6a and 6b are also described). The variants have a modified  
 CC affinity for matrix and low affinity receptors. This alters the  
 CC bioavailability of the proteins when administered directly to cells.  
 CC These variants are used to treat vascular disease, especially  
 CC cardiovascular disease, by stimulating vascular cell proliferation. They  
 CC enhance epithelialisation of diseased vessels, especially after  
 CC angioplasty. The re-endothelialisation reduces or prevents restenosis.  
 CC They are also useful for enhancing drug permeation by tumours and for  
 CC treating ischemic conditions such as cardiac infarction, chronic coronary  
 CC ischemia, chronic lower limb ischemia, stroke and peripheral vascular  
 CC disease. In addition they may be used to treat wounds.  
 XX  
 XX Sequence 188 AA;  
 SQ  
 Query Match 100.0%; Score 792; DB 20; Length 188;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-75;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLLSVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLLSVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 DB 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 14  
 AAW62525  
 ID AAW62525 standard; Protein; 191 AA.  
 XX  
 XX AAW62525;  
 AC  
 XX 11-SEP-1998 (first entry)  
 DT



XX		Amino acid sequence of human VEGF-165.
DE		
XX		
KW	Human; vascular endothelial growth factor; VEGF; production;	
KW	nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;	
KW	blood vessel; essential hypertension; pulmonary arterial hypertension;	
KW	PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;	
KW	coronary bypass operation; anastomosis; endarterectomy.	
OS		
XX	Homo sapiens.	
XX		
PX	WO9820027-A2.	
XX		
PD	14-MAY-1998.	
XX		
XX	03-NOV-1997; 97WO-GB03015.	
PF		
XX		
PR	21-AUG-1997; 97GB-0017791.	
PR	01-NOV-1996; 96GB-0022852.	
PR	09-MAY-1997; 97GB-0009494.	
XX		
XX	(EURO-) EUROGENE LTD.	
PI		
PI	Barker SGE, Martin JF, Yla-Herttuala S;	
XX		
DR	WPI; 1998-286857/25.	
DR	N-PSDB; AAV38451.	
XX		
PT	Treatment or prevention of intimal hyperplasia by stimulating	
PT	production of nitric oxide - By administration of vascular	
PT	endothelial growth factor, useful for, e.g. treating or preventing	
PT	intimal hyperplasia	
XX		
PS	Claim 8; Pages 56-57; 70pp; English.	
XX		
CC	The present sequence represents human vascular endothelial growth factor	
CC	165 (VEGF-165). VEGF stimulates production of nitric oxide and	
CC	prostacyclin. VEGF can therefore be used for treatment or prevention	
CC	of intimal hyperplasia in a blood vessel. VEGF can be used for treating	
CC	or preventing any condition responsive to in vivo stimulation of	
CC	nitric acid and prostacyclin (especially essential hypertension,	
CC	pulmonary arterial hypertension (PAH), cor pulmonale and	
CC	atherosclerosis. VEGF is specifically used to control (re)stenosis,	
CC	where caused by PAH or by a surgical procedure such as angioplasty,	
CC	coronary bypass operation, anastomosis or endarterectomy.	
XX		
SQ	Sequence 191 AA;	
Query Match 100.0%; Score 792; DB 19; Length 191;		
Best Local Similarity 100.0%; Pred. No. 1.1e-75;		
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps		
QY	1 MNFLLSVHWHS LALLYLHLHAKWSQAAPMAEGGGQHHEVVKFMDVYQRSYCHPIETLVD 60	
Db		
Db	1 MNFLLSVHWHS LALLYLHLHAKWSQAAPMAEGGGQHHEVVKFMDVYQRSYCHPIETLVD 60	
QY	61 IFQEYPDEI EYIFKPCVPLMRGCGCNDBGLECVPTESNITMQIMRTKPHOGOHIGEM 120	
Db		
Db	61 IFQEYPDEI EYIFKPCVPLMRGCGCNDBGLECVPTESNITMQIMRTKPHOGOHIGEM 120	
QY	121 SFLOHNKCECRPKKDRARQEK 141	
Db		
Db	121 SFLOHNKCECRPKKDRARQEK 141	
RESULT 15		
AAV43483		
ID	AAV43483 standard; Protein; 208 AA.	
XX		
AC	AAV43483;	
XX		
DT	26-JAN-2000 (first entry)	
XX		

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 04:56:43 ; Search time 51 Seconds  
(without alignments)  
43.299 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLOHNKCECRPKKDRARQEK 141

Scoring table: BLOSUM62

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Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep.\*

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10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep.\*

11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*

12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep.\*

13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	792	100.0	171	10	US-09-812-133-2
2	792	100.0	215	10	US-09-244-694-3
3	792	100.0	232	10	US-09-795-006A-147
4	792	100.0	232	12	US-10-127-551-5
5	787	99.4	191	10	US-09-349-954A-2
6	787	99.4	191	10	US-09-932-451A-2
7	787	99.4	191	10	US-09-907-007-2
8	787	99.4	191	10	US-09-795-006A-2
9	787	99.4	192	9	US-09-852-209A-8
10	686.5	86.7	214	10	US-09-349-954A-22
11	686.5	86.7	214	10	US-09-907-007-22
12	645	81.4	190	9	US-09-813-398-8
13	621	78.4	110	10	US-09-822-270-17
14	583	73.6	126	10	US-09-795-006A-43
15	531	67.0	94	10	US-09-761-636A-2
16	521.5	65.8	127	10	US-09-795-006A-83
17	516	65.2	105	10	US-09-925-299-927
18	512.5	64.7	127	10	US-09-795-006A-87
19	506	63.9	105	10	US-09-795-006A-51

20	501	63.3	126	10	US-09-795-006A-55	Sequence 55, Appl
21	474.5	59.9	127	10	US-09-795-006A-91	Sequence 91, Appl
22	465.5	58.8	127	10	US-09-795-006A-95	Sequence 95, Appl
23	460.5	58.1	127	10	US-09-795-006A-85	Sequence 85, Appl
24	459	58.0	105	10	US-09-795-006A-59	Sequence 59, Appl
25	454	57.3	126	10	US-09-795-006A-63	Sequence 63, Appl
26	452	57.1	105	10	US-09-795-006A-153	Sequence 153, Appl
27	451.5	57.0	127	10	US-09-795-006A-89	Sequence 89, Appl
28	451	56.9	79	9	US-10-086-623-14	Sequence 14, Appl
29	449.5	56.8	105	10	US-09-795-006A-161	Sequence 161, Appl
30	449	56.7	126	10	US-09-795-006A-53	Sequence 53, Appl
31	445.5	56.2	129	10	US-09-795-006A-99	Sequence 99, Appl
32	440	55.6	126	10	US-09-795-006A-57	Sequence 57, Appl
33	436.5	55.1	129	10	US-09-795-006A-103	Sequence 103, Appl
34	434	54.8	128	10	US-09-795-006A-67	Sequence 67, Appl
35	425	53.7	128	10	US-09-795-006A-71	Sequence 71, Appl
36	415	52.4	105	10	US-09-795-006A-173	Sequence 173, Appl
37	413.5	52.2	127	10	US-09-795-006A-93	Sequence 93, Appl
38	413	52.1	105	10	US-09-795-006A-163	Sequence 163, Appl
39	406	51.3	105	10	US-09-795-006A-175	Sequence 175, Appl
40	404.5	51.1	127	10	US-09-795-006A-97	Sequence 97, Appl
41	402	50.8	126	10	US-09-795-006A-61	Sequence 61, Appl
42	398.5	50.3	129	10	US-09-795-006A-107	Sequence 107, Appl
43	393	49.6	105	10	US-09-795-006A-165	Sequence 165, Appl
44	393	49.6	126	10	US-09-795-006A-65	Sequence 65, Appl
45	390	49.2	128	10	US-09-795-006A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1

US-09-812-133-2  
; Sequence 2, Application US/09812133  
; Patent No. US20020065240A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Kenneth A., Jr.  
; APPLICANT: Kendall, Richard L.  
; APPLICANT: Bett, Andrew J.  
; APPLICANT: Huckle, William R.  
; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF ANGIOGENESIS  
; FILE REFERENCE: 20073P  
; CURRENT APPLICATION NUMBER: US/09/812,133  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: PCT/US98/22668  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/063,629  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID, NO 2  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Human  
US-09-812-133-2

Query Match	100.0%;	Score	792;	DB	10;	Length	171;
Best Local Similarity	100.0%;	Pred. No.	1.4e-75;				
Matches	141;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MNFLSWHWSLALLLYLHHAKWSQAAPMAEGGQNHHEVVVKFMDVYORSYCHPIETLVD	60				
Db	1	MNFLSWHWSLALLLYLHHAKWSQAAPMAEGGQNHHEVVVKFMDVYORSYCHPIETLVD	60				
QY	61	IFQEYPDIEYIFKPSVCPMLRCGCCNDGECVPTESNITMIMRKPHQGHIGEM	120				
Db	61	IFQEYPDIEYIFKPSVCPMLRCGCCNDGECVPTESNITMIMRKPHQGHIGEM	120				
QY	121	SFLOHNKCECRPKKDRARQEK	141				
Db	121	SFLOHNKCECRPKKDRARQEK	141				

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RESULT 2
US-09-244-694-3
; Sequence 3, Application US/09244694
; Patent No. US2002026037A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Olsen, Henrik S.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 3
; FILE REFERENCE: 1488.1040003
; CURRENT APPLICATION NUMBER: US/09/244,694
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 09/132,088
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/033,662
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: US 08/469,641
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-694-3

Query Match      100.0%; Score 792; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
Db 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
QY 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
Db 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLQHNKCECRPKKDRARQEK 141
Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 3
US-09-795-006A-147
; Sequence 147, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 147
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-147

Query Match      100.0%; Score 792; DB 10; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
Db 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
QY 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
Db 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLQHNKCECRPKKDRARQEK 141
Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 4
US-10-127-551-5
; Sequence 5, Application US/10127551
; Patent No. US20020120123A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: PF112P1
; CURRENT APPLICATION NUMBER: US/10/127,551
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/465,968
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/207,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-551-5

Query Match      100.0%; Score 792; DB 12; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
Db 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
QY 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
Db 61 IFQEYDPEIEYIFKPCVPLMRCGCCNDGEGLECYPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLQHNKCECRPKKDRARQEK 141
Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 5
US-09-349-954A-2
; Sequence 2, Application US/09349954A
; Patent No. US20020019027A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020019027Aldenskjold, Magnus
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: Dav. Col. Cave
; CURRENT APPLICATION NUMBER: US/09/349,954A
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Nucleotide Sequence of VEGF165
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## US-09-349-954A-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 6

US-09-932-451A-2  
; Sequence 2, Application US/09932451A  
; Patent No. US20020111324A1  
; GENERAL INFORMATION:  
; APPLICANT: OZAWA, Kelya  
; APPLICANT: SHIMPO, Masahisa  
; APPLICANT: IKEDA, Uichi  
; APPLICANT: MAEDA, Yoshikazu  
; APPLICANT: SHIMADA, Kazuyuki  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC  
; FILE REFERENCE: 0800-0026  
; CURRENT APPLICATION NUMBER: US/09/932,451A  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,056  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-165

## US-09-932-451A-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 7

US-09-907-007-2  
; Sequence 2, Application US/09907007  
; Patent No. US20020142395A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayward, Nicholas K.  
; APPLICANT: Weber, Gunther  
; APPLICANT: Grimmond, Sean  
; APPLICANT: No. US20020142395A1denskjold, Magnus  
; APPLICANT: Larsson, Catharina

; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
; FILE REFERENCE: SAME  
; FILE REFERENCE: DAVIES  
; CURRENT APPLICATION NUMBER: US/09/907,007  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 08/765,588  
; PRIOR FILING DATE: 1996-02-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Nucleotide Sequence of VEGF165  
US-09-907-007-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 8

US-09-795-006A-2  
; Sequence 2, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-006A-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQGQHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 9



QY	42	KFMDVQRSYCHPIETLVDIFQYDEIEYIFKPSVPLMRGCGCNDGSELCVPTESN	101
Db	1	KFMDVQRSYCHPIETLVDIFQYDEIEYIFKPSVPLMRGCGCNDGSELCVPTESN	60
QY	102	ITWIMRIKPHOGHIGEMSFLOHNKCECRPKD	135

Db 61 :|||||||||||||||||||||||||||||||||||||  
LTMQIMRIKPHQGHIGEMSFOHNKCECRPKD 94

Search completed: November 20, 2002, 05:01:37  
Job time : 52 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 04:55:04 ; Search time 45 Seconds  
(without alignments)  
301.221 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLOHNRCEPRKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	100.0	232	2 A41551	vascular endotheli
2	733.5	92.6	190	2 S52130	vascular endotheli
3	719.5	90.8	146	2 S57956	ovine vascular end
4	717.5	90.6	190	2 B40080	vascular endotheli
5	686.5	86.7	214	2 A44881	vascular endotheli
6	681.5	86.0	190	2 B44881	vascular endotheli
7	680.5	85.9	190	2 A35987	glioma-derived vas
8	575.5	72.7	120	2 A33787	vascular endotheli
9	367.5	46.4	128	2 I51295	vascular endotheli
10	325	41.0	149	2 A41236	placental growth f
11	294	37.1	158	2 A56125	placental growth f
12	264	33.3	188	2 JC4680	vascular endotheli
13	264	33.3	207	2 JC4679	vascular endotheli
14	237	29.9	133	2 B49530	vascular endotheli
15	192	24.2	419	2 S69207	vascular endotheli
16	163	20.6	148	2 D49530	16K vascular endot
17	137.5	17.4	36	2 A60706	vascular endotheli
18	99.5	12.6	226	1 TVMVSS	PDGF-related trans
19	99.5	12.6	241	1 PFHUG2	platelet-derived g
20	99.5	12.6	245	1 TVCTSS	platelet-derived g
21	96.5	12.2	200	2 I51551	platelet-derived g
22	96.5	12.2	215	2 S08220	platelet-derived g
23	96.5	12.2	226	2 I51550	platelet-derived g
24	95	12.0	211	1 PFHUG1	platelet-derived g
25	94.5	11.9	166	2 JN0248	platelet-derived g
26	94.5	11.9	196	2 B28964	platelet-derived g
27	94.5	11.9	196	2 A48851	platelet-derived g
28	94.5	11.9	197	2 S25096	platelet-derived g
29	94.5	11.9	198	2 JS0735	platelet-derived g

#### ALIGNMENTS

##### RESULT 1

A41551

vascular endothelial growth factor 206 precursor - human  
N:Alternate names: vascular permeability factor  
N:Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VE

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1992 #sequence.revision 28-Aug-1992 #text.change 05-Nov-1999  
C:Accession: A41551; B41551; A40454; B40454; A40079; A40080; JQ1463

R:Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.

Mol. Endocrinol. 5, 1806-1814, 1991

A:Title: The vascular endothelial growth factor family: identification of a fourth mo  
A:Reference number: A41551; MUID:92168017; PMID:1791831

A:Accession: A41551

A:Molecule type: mRNA

A:Residues: 1-232 <H0U1>

A:Cross-references: GB:S85192; NID:g246155; PID:g246156

A:Accession: C41551

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-140, 'N', 183-232 <H0U2>

A:Accession: B41551

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-141, 227-232 <H0U>

R:Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;

J. Biol. Chem. 266, 11947-11954, 1991

A:Title: The human gene for vascular endothelial growth factor. Multiple protein form

A:Reference number: A40454; MUID:91268072; PMID:1711045

A:Accession: A40454

A:Molecule type: DNA

A:Residues: 1-165, 183-232 <T11>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;

A:Accession: B40454

A:Molecule type: DNA

A:Residues: 1-140, 'N', 183-232 <T12>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977;

A:Accession: C40454

A:Molecule type: DNA

A:Residues: 1-141, 227-232 <T13>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978

R:Kek, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.

Science 246, 1309-1312, 1989

A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.

A:Reference number: A40079; MUID:90069609; PMID:2479987

A:Accession: A40079

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-165, 183-232 <KEC>

A:Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301

R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.

Science 246, 1306-1309, 1989

A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.

A:Reference number: A40080; MUID:90069608; PMID:2479986  
A:Accession: A40080  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <LEU>  
A:Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971  
R:Weindel, K.; Marne, D.; Welch, H.A.  
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992  
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial  
A:Reference number: JQ1463; MUID:92231879; PMID:1567395  
A:Accession: JQ1463  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <WEI>  
A:Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659  
A:Experimental source: AIDS-Kaposi's sarcoma cell  
A:Accession: JQ1464  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 227-232 <WE2>  
A:Experimental source: AIDS-Kaposi's sarcoma cell  
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay  
J. Biol. Chem. 264, 20017-20024, 1989  
A:Title: Human vascular permeability factor. Isolation from U937 cells.  
A:Reference number: A34492; MUID:90062112; PMID:2584205  
A:Accession: A34492  
A:Molecule type: protein  
A:Residues: 27-36; 43-49, 'R', 72-76, 'Q', 78-81; 59-71 <CON>  
C:Comment: The most common of several alternatively spliced forms is VEGF 165.  
C:Genetics:  
A:Gene: GDB:VEGF  
A:Cross-references: GDB:132244; OMIM:192240  
A:Map position: 6p21-6p12  
C:Function:  
A:Description: promotes fluid and protein leakage from blood vessels  
A:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro  
F:1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20  
F:1-165, 183-232/Product: vascular endothelial growth factor 189 precursor #status predic  
F:1-141, 227-232/Product: vascular endothelial growth factor 121 precursor #status predic  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9e-73;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||

QY 121 SFLOHNKCECRPKDKAROEK 141  
|||||  
Db 121 SFLOHNKCECRPKDKAROEK 141  
|||||

RESULT 2  
S52130  
vascular endothelial growth factor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999  
C:Accession: S52130  
R:Sharma, H.S.; Tang, Z.H.; Cho, B.C.G.; Verdouw, P.D.  
Biochim. Biophys. Acta 1260, 235-238, 1995  
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth  
A:Reference number: S52130; MUID:95143284; PMID:7841203  
A:Accession: S52130  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-190 <SHA>  
A:Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 92.6%; Score 733.5; DB 2; Length 190;  
Best Local Similarity 95.7%; Pred. No. 6.2e-67;  
Matches 134; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GGQKPHEVVFMDVYQSYCHPIETLVD 59  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||  
Db 60 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 119  
|||||

QY 121 SFLOHNKCECRPKDKAROEK 140  
|||||  
Db 120 SFLOHNKCECRPKDKAROEK 139  
|||||

RESULT 3  
S57956  
ovine vascular endothelial growth factor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: S57956  
R:Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S57956  
A:Accession: S57956  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <RED>  
A:Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351

Query Match 90.8%; Score 719.5; DB 2; Length 146;  
Best Local Similarity 92.2%; Pred. No. 1.2e-65;  
Matches 130; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GGQKPHEVVFMDVYQSYCHPIETLVD 59  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||  
Db 60 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGQHIGEM 119  
|||||

QY 121 SFLOHNKCECRPKDKAROEK 141  
|||||  
Db 120 SFLOHNKCECRPKDKAROEK 140  
|||||

RESULT 4  
B40080  
vascular endothelial growth factor precursor (version 2) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 05-Nov-1999  
C:Accession: B40080; B33787; A33255  
R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.  
Science 246, 1306-1309, 1989  
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.  
A:Reference number: A40080; MUID:90069608; PMID:2479986  
A:Accession: B40080  
A:Molecule type: mRNA  
A:Residues: 1-190 <LEU>  
A:Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007  
R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr  
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989  
A:Title: Vascular endothelial growth factor: a new member of the platelet-derived gro  
A:Reference number: A33787; MUID:90121225; PMID:2610687  
A:Accession: B33787  
A:Molecule type: mRNA  
A:Residues: 27-190 <TIS>  
A:Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809  
R:Ferrara, N.; Henzel, W.J.  
Biochem. Biophys. Res. Commun. 161, 851-858, 1989

A>Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specific  
 A:Reference number: A33255; MUID:89286596; PMID:2735925  
 A:Accession: A33255  
 A:Molecule type: protein  
 A:Residues: 27-31 <FER>  
 C:Keywords: alternative splicing; glycoprotein  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-190/Product: vascular endothelial growth factor #status predicted <MAT>  
 F:100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.6%; Score 717.5; DB 2; Length 190;  
 Best Local Similarity 92.9%; Pred. No. 2.6e-65;  
 Matches 130; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GGQPHVVKFMDVYORSYCHPIETLVD 59  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQSGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQSGHIGEM 119  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 121 SFLQHNKCECRPKKDRARQE 140  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 SFLQHNKCECRPKKDRARQE 139  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5  
 A44881  
 vascular endothelial growth factor-3 precursor - mouse  
 N:Contains: vascular endothelial growth factor-2; vascular permeability factor  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
 C:Accession: A44881; A60932; S52136  
 R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.  
 Development 114, 521-532, 1992  
 A>Title: Expression of vascular endothelial growth factor during embryonic angiogenesis  
 A:Reference number: A44881; MUID:92274860; PMID:1592003  
 A:Accession: A44881  
 A:Molecule type: mRNA  
 A:Residues: 1-214 <BRE>  
 A:Cross-references: GB:S37052; NID:g249856; PIDN:AB22252.1; PID:g249857  
 A:Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)  
 A:Accession: C44881  
 A:Molecule type: protein  
 A:Residues: 1-140, 209-214 <BR2>  
 A:Cross-references: GB:S38100; NID:g249860; PIDN:AB22254.1; PID:g249861  
 A:Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIP:107625)  
 R:Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.  
 J. Exp. Med. 172, 1535-1545, 1990  
 A>Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothelial  
 A:Reference number: A60932; MUID:91079755; PMID:2258694  
 A:Accession: A60932  
 A:Molecule type: protein  
 A:Residues: 27-33 <CLA>  
 R:Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.  
 Biochim. Biophys. Acta 1224, 365-370, 1994  
 A>Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous in  
 A:Reference number: S52136; MUID:95101726; PMID:7803491  
 A:Accession: S52136  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-46 <SUG>  
 C:Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.  
 C:Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match 86.7%; Score 686.5; DB 2; Length 214;  
 Best Local Similarity 87.2%; Pred. No. 4.1e-62;  
 Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPTE-GEQKSHEVVKFMDVYORSYCHPIETLVD 59  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQSGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEALECVPTESNITMIMRIKPHQSGHIGEM 119  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 121 SFLQHNKCECRPKKDRARQE 141  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 SFLQHSRCECRPKKDRTRPEK 140  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6  
 B44881  
 vascular endothelial growth factor-1 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Nov-1999  
 C:Accession: B44881; A43351; A61029  
 R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.  
 Development 114, 521-532, 1992  
 A>Title: Expression of vascular endothelial growth factor during embryonic angiogenesis  
 A:Reference number: A44881; MUID:92274860; PMID:1592003  
 A:Accession: B44881  
 A:Molecule type: mRNA  
 A:Residues: 1-190 <BRE>  
 A:Cross-references: GB:S38083; NID:g249858; PIDN:AB22253.1; PID:g249859  
 A:Experimental source: embryo  
 A:Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)  
 R:Claiffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.  
 J. Biol. Chem. 267, 16317-16322, 1992  
 A>Title: Vascular endothelial growth factor. Regulation by cell differentiation and a  
 A:Reference number: A43351; MUID:92355593; PMID:1644816  
 A:Accession: A43351  
 A:Molecule type: mRNA  
 A:Residues: 1-116, 191-190 <CLA>  
 A:Cross-references: GB:M95200; NID:g202350; PIDN:AAA0547.1; PID:g202351  
 A:Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)  
 R:Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.  
 Growth Factors 4, 53-59, 1990  
 A>Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial  
 A:Reference number: A61029; MUID:91197543; PMID:2085441  
 A:Accession: A61029  
 A:Molecule type: protein  
 A:Residues: 27-38 <ROS>  
 C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;

Query Match 86.0%; Score 681.5; DB 2; Length 190;  
 Best Local Similarity 87.1%; Pred. No. 1.2e-61;  
 Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPTE-GEQKSHEVVKFMDVYORSYCHPIETLVD 59  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHQSGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEALECVPTESNITMIMRIKPHQSGHIGEM 119  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 121 SFLQHNKCECRPKKDRARQE 140  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 SFLQHSRCECRPKKDRTRPE 139  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7  
 A35987  
 glioma-derived vascular endothelial cell growth factor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 05-Nov-1999  
 C:Accession: A35987  
 R:Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Ho  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990  
 A>Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is

A:Reference number: A35987; MUID:90207249; PMID:2320579

A:Accession: A35987

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-190 <CON>

A:Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

Query Match 85.9%; Score 680.5; DB 2; Length 190;  
Best Local Similarity 87.1%; Pred. No. 1.5e-61;  
Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSWHSLALLYLHAKVQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60

DB 1 MNFLLSWHSLALLYLHAKVQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59

QY 61 IFQEYDEIEYIFKPSVPLMRGCGCNDGEGLECVPTESNITMQIMRIKPHQGHIGEM 120

DB 60 IFQEYDEIEYIFKPSVPLMRGCGCNDGEGLECVPTESNITMQIMRIKPHQGHIGEM 119

QY 121 SFLQHNKCECRPKKDRQEK 140

DB 120 SFLQHSRCECRPKKDRKPE 139

RESULT 8

A33787

vascular endothelial growth factor (version 1) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 05-Nov-1999

C:Accession: A33787

R:Rischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp

Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989

A:Title: Vascular endothelial growth factor: a new member of the platelet-derived growth

A:Reference number: A33787; MUID:90121225; PMID:2610687

A:Accession: A33787

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <TIS>

A:Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:g163811

C:Keywords: alternative splicing

Query Match

Best Local Similarity 72.7%; Score 575.5; DB 2; Length 120;

Matches 105; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 27 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDEIEYIFKPSVPLMRGCGC 86

DB 1 APMAE-GGQKPHEVVKFMDVYQSYCHPIETLVDIFQEYDEIEYIFKPSVPLMRGCGC 59

QY 87 CNDEGLECVPTESNITMQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRQEK 141

DB 60 CNDEGLECVPTESNITMQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRQEK 114

RESULT 9

I51295

vascular endothelial growth factor - quail (fragment)

C:Species: Phasianidae gen. sp. (quail)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 28-Feb-1997

C:Accession: I51295

R:Flamme, I.; Breier, G.; Risau, W.

Dev. Biol. 169, 699-712, 1995

A:Title: Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1) are expres

A:Reference number: I51295; MUID:95301109; PMID:7781909

A:Accession: I51295

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-128 <FLA>

A:Cross-references: GB:S78343; NID:g999147; PID:g999148

C:Genetics:

A:Gene: VEGF

Query Match 46.4%; Score 367.5; DB 2; Length 128;

Best Local Similarity 75.9%; Pred. No. 5.2e-30;

Matches 63; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 60 DIFQEYDEIEYIFKPSVPLMRGCGCNDGEGLECVPTESNITMQIMRIKPHQGHIGCE 119

DB 1 DIFQEYDEIEYIFRPSVPLMRGCGCNDGEGLECVPTDVYNTMETARIKPHQSHIAH 60

QY 120 MSFLOHNKCECRPKKDRQEK 141

DB 61 MSFLOHSHKCDCKRPKDKVKNKQEK 83

RESULT 10

A41236

placental growth factor precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 05-Nov-1999

C:Accession: A41236

R:Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, P.; Persico, M.G.

Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991

A:Title: Isolation of a human placenta cDNA coding for a protein related to the vascu

A:Reference number: A41236; MUID:92021031; PMID:1924389

A:Accession: A41236

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <MAG>

A:Cross-references: GB:X54936; NID:g35521; PIDN:CAA38698.1; PID:g35522

C:Genetics:

A:Gene: GDB:PGF

A:Cross-references: GDB:I34676; OMIM:601121

A:Map position: 14q24-14q31

Query Match

Best Local Similarity 41.0%; Score 325; DB 2; Length 149;

Matches 55; Conservative 26; Mismatches 35; Indels 4; Gaps 1;

QY 22 KWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDEIEYIFKPSVPLM 81

DB 26 QWALSA----GNGSSEVVVPEQVWGRSYCRALERLVDWSEYPSVEHEMFSPSCVSL 81

QY 82 RGGCGCNDGEGLECVPTESNITMQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRQEK 141

DB 82 RCTGCGGDNHLCVPVETANTVMQLKIRSGDRPSVELTFSQHVRCERPLREKMKPER 141

RESULT 11

A56125

placental growth factor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 05-Nov-1999

C:Accession: A56125

R:DiSalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; Soderman, D.D.; Pall

J. Biol. Chem. 270, 7717-7723, 1995

A:Title: Purification and characterization of a naturally occurring vascular endothel

A:Reference number: A56125; MUID:95221439; PMID:7706320

A:Accession: A56125

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-158 <DIS>

A:Cross-references: GB:L40030; NID:gl263413; PIDN:AAA97426.1; PID:gl263414

C:Keywords: glycoprotein

Query Match

Best Local Similarity 37.1%; Score 294; DB 2; Length 158;

Matches 58; Conservative 19; Mismatches 40; Indels 2; Gaps 2;

QY 24 SQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDEIEYIFKPSVPLMRC 83

DB 21 SQGA-LSAGNNSTEMEVVPEVWGRSYCRPMKLVYIADEHPNEVSHIFSPCVLLSRC 79

QY 84 GCGCNDGEGLECVPTESNITMQIMRIKPHQGH-IGEMSFLOHNKCECRPKKDRQEK 141

DB 80 SGCCGDEGLHCVALKTANTITMQLKIPPNRDPHSVEMTFSQDVLCECRPILETTKAER 138

RESULT 12  
JC4680  
vascular endothelial growth factor-related factor 167 precursor - mouse  
N:Alternate names: VRF 167 protein  
C:Species: Mus musculus (house mouse)  
C:Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: JC4680  
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.;  
Biochem. Biophys. Res. Commun. 220, 922-928, 1996  
A:Title: Characterization of the murine VEGF-related factor gene.  
A:Reference number: JC4679; MUID:96183052; PMID:8607868  
A:Accession: JC4680  
A:Molecule type: mRNA  
A:Residues: 1-188 <TOW>  
A:Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336  
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs  
ar endothelial growth factors 167 and VEGF 186.  
C:Genetics:  
A:Gene: vrf  
A:Map position: 19  
A:Introns: 137/2  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-188/Product: vascular endothelial growth factor-related factor #status predicted <V>  
  
Query Match 33.3%; Score 264; DB 2; Length 188;  
Best Local Similarity 42.7%; Pred. No. 2.4e-19;  
Matches 53; Conservative 23; Mismatches 42; Indels 6; Gaps 3;  
  
Qy 12 LALLYLHAKWSQAAPMAEGGQNH-EVVKFMDVQSRCHPTIETLVDFIQEYVPDRIE 70  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 10 LVALLQLARTQ----APVSQDGPESHQKVVVPWIDVYARATCQPREVVVPLSMELMGNNV 65  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 71 YIFKPSVPLMRGCGCCNDGEGLECVPTESNTITQIMRIKPHOGHIGEMSFLOHKNKEC 130  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 66 KQLVPSCVTVQRCGCCPDGEGLECVPTGQHQRVMOILMIQ-YPSSQLGEMSLSEHSQCEC 124  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 131 RPKK 134  
| | | |  
Db 125 RPKK 128  
| | | |  
  
RESULT 13  
JC4679  
vascular endothelial growth factor-related factor 186 precursor - mouse  
N:Alternate names: VRF 186 protein, VEGF 186  
C:Species: Mus musculus (house mouse)  
C:Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: JC4679  
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.;  
Biochem. Biophys. Res. Commun. 220, 922-928, 1996  
A:Title: Characterization of the murine VEGF-related factor gene.  
A:Reference number: JC4679; MUID:96183052; PMID:8607868  
A:Accession: JC4679  
A:Molecule type: mRNA  
A:Residues: 1-207 <TOW>  
A:Cross-references: GB:U43836; NID:g1703480; PIDN:AAC52932.1; PID:g1314334  
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs  
lar endothelial growth factors 167 and 186.  
C:Genetics:  
A:Gene: vrf  
A:Map position: 19  
A:Introns: 137/2  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-207/Product: vascular endothelial growth factor-related factor #status predicted <V>  
  
Query Match 33.3%; Score 264; DB 2; Length 207;  
Best Local Similarity 42.7%; Pred. No. 2.6e-19;  
Matches 53; Conservative 23; Mismatches 42; Indels 6; Gaps 3;  
  
Qy 12 LALLYLHAKWSQAAPMAEGGQNH-EVVKFMDVQSRCHPTIETLVDFIQEYVPDRIE 70  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 10 LVALLQLARTQ----APVSQDGPESHQKVVVPWIDVYARATCQPREVVVPLSMELMGNNV 65  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 71 YIFKPSVPLMRGCGCCNDGEGLECVPTESNTITQIMRIKPHOGHIGEMSFLOHKNKEC 130  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 66 KQLVPSCVTVQRCGCCPDGEGLECVPTGQHQRVMOILMIQ-YPSSQLGEMSLSEHSQCEC 124  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 131 RPKK 134  
| | | |  
Db 125 RPKK 128  
| | | |

Db 10 LVALLQLARTQ----APVSQDGPESHQKVVVPWIDVYARATCQPREVVVPLSMELMGNNV 65  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 71 YIFKPSVPLMRGCGCCNDGEGLECVPTESNTITQIMRIKPHOGHIGEMSFLOHKNKEC 130  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 66 KQLVPSCVTVQRCGCCPDGEGLECVPTGQHQRVMOILMIQ-YPSSQLGEMSLSEHSQCEC 124  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 131 RPKK 134  
| | | |  
Db 125 RPKK 128  
| | | |  
  
RESULT 14  
B49530  
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus  
C:Species: Orf virus  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: B49530  
R:Lytile, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.  
J. Virol. 68, 84-92, 1994  
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o  
A:Reference number: A49530; MUID:94076465; PMID:8254780  
A:Contents: NZ2  
A:Accession: B49530  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <LYT>  
A:Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)  
  
Query Match 29.9%; Score 237; DB 2; Length 133;  
Best Local Similarity 44.9%; Pred. No. 9e-17;  
Matches 40; Conservative 17; Mismatches 32; Indels 0; Gaps 0;  
  
Qy 45 DVYQSRCHPTIETLVDFIQEYVPDRIEYIFKPSVPLMRGCGCCNDGEGLECVPTESNTITM 104  
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Db 29 EVLKGSKRPPIVVPVSETHPELTQSRFPNPPCVTLMRCGCCNDGEGLECVPTESNTITM 88  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Qy 105 QIMRIKPHOGHIGEMSFLOHKNKECRPK 133  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
Db 89 ELLGASGSGSNGMQRSLSFVEHKKDCRPR 117  
| | | | : | | | : | | | : | | | : | | | : | | | : | | | :  
  
RESULT 15  
S69207  
vascular endothelial growth factor C precursor - human  
N:Alternate names: FLT4 ligand DHM  
C:Species: Homo sapiens (man)  
C:Date: 27-Apr-1996 #sequence\_revision 01-Nov-1996 #text\_change 08-Oct-1999  
C:Accession: S69207; S61795; S71443; S69208; G02659  
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksel  
EMBO J. 15, 1751, 1996  
A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand  
A:Reference number: S69207; MUID:96203094; PMID:8612600  
A:Accession: S69207  
A:Status: nucleic acid sequence not shown  
A:Residues: 1-419 <JOU>  
A:Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995  
A:Note: only a part of the translation is shown  
A:Note: this is a revision to the sequence from reference S61795  
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksel  
EMBO J. 15, 290-298, 1996  
A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4  
A:Reference number: S61795; MUID:96178224; PMID:8617204  
A:Accession: S61795  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 70-419 <JOU>  
A:Note: this sequence has been revised in reference S69207  
A:Accession: S71443  
A:Molecule type: protein



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OM protein - protein search, using sw model

Run on: November 20, 2002, 03:30:52 ; Search time 28 Seconds  
(without alignments)  
208.863 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWVHWSLALLYLHH.....FLQHNKCEPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	792	100.0	232	1 VEGA_HUMAN	P15692 homo sapien
2	733.5	92.6	190	1 VEGA_PIG	P49151 sus scrofa
3	728.5	92.0	214	1 VEGA_CANFA	Q9myv3 canis famil
4	719.5	90.8	146	1 VEGA_SHEEP	P50412 ovis aries
5	717.5	90.6	190	1 VEGA_BOVIN	P15691 bos taurus
6	708.5	89.5	190	1 VEGA_HORSE	Q9gkr0 equus cabal
7	686.5	86.7	214	1 VEGA_MOUSE	Q00731 mus musculus
8	685.5	86.6	214	1 VEGA_RAT	P16612 rattus norv
9	665.5	84.0	190	1 VEGA_MESAU	Q99psi mesocricetu
10	555.5	70.1	216	1 VEGA_CHICK	P52582 gallus gall
11	543.5	68.6	164	1 VEGA_CAVPO	P26617 cavia porce
12	320	40.4	149	1 PLGF_BOVIN	Q9xs47 bos taurus
13	314	39.6	158	1 PLGF_MOUSE	P49764 bos musculus
14	308	38.9	221	1 PLGF_HUMAN	P49763 homo sapien
15	294	37.1	158	1 PLGF_RAT	P63434 rattus norv
16	267.5	33.8	207	1 VEGB_BOVIN	Q9xs49 bos taurus
17	265.5	33.5	207	1 VEGB_HUMAN	P49765 homo sapien
18	264	33.3	207	1 VEGB_MOUSE	P49766 mus musculus
19	240.5	30.4	135	1 VEGB_RAT	O35485 rattus norv
20	233	29.4	133	1 VEGB_ORFN2	P52584 orf virus (
21	192	24.2	419	1 VEGC_HUMAN	P49767 homo sapien
22	184.5	23.3	415	1 VEGC_MOUSE	P97953 mus musculus
23	172.5	21.8	358	1 VEGD_MOUSE	P97946 mus musculus
24	169.5	21.4	354	1 VEGD_HUMAN	O43915 homo sapien
25	166.5	21.0	326	1 VEGD_RAT	O35251 rattus norv
26	163	20.6	148	1 VEGD_ORFN7	P52585 orf virus (
27	122	15.4	126	1 VEGC_RAT	O35757 rattus norv
28	110.5	14.0	241	1 PGCB_SHEEP	Q95229 ovis aries
29	99.5	12.6	226	1 TSFS_SMSAV	P01128 simian sarc
30	99.5	12.6	241	1 PGCB_HUMAN	P01127 homo sapien
31	99.5	12.6	245	1 PGCB_FELCA	P12919 felis silve
32	96.5	12.2	226	1 PDGA_XENLA	P13698 xenopus lae
33	95	12.0	211	1 PDGA_HUMAN	P04085 homo sapien

## RESULT 1

ID	VEGA_HUMAN	STANDARD;	PRT;	232 AA.
AC	P15692; Q16889; Q60720; Q75875; Q9UL23; Q9UH58; Q9H1W9; Q9H1W8;			
AC	Q96NW5;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).			
DE	VEGF OR VEGFA.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).			
RX	MEDLINE=90069608; PubMed=2479986;			
RA	Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;			
RT	"Vascular endothelial growth factor is a secreted angiogenic mitogen.";			
RT	Science 246:1306-1309(1989).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.			
RP	MEDLINE=90069609; PubMed=2479987;			
RA	Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J., Connolly D.T.;			
RT	"Vascular permeability factor, an endothelial cell mitogen related to PDGF.";			
RT	Science 246:1309-1312(1989).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF189).			
RP	MEDLINE=91268072; PubMed=1711045;			
RX	Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D., Fiddes J.C., Abraham J.A.;			
RA	"The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing.";			
RT	J. Biol. Chem. 266:11947-11954(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM VEGF206).			
RX	MEDLINE=92168017; PubMed=1791831;			
RA	Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;			
RT	"The vascular endothelial growth factor family: identification of a fourth molecular species and characterization of alternative splicing of RNA.";			
RT	Mol. Endocrinol. 5:1806-1814(1991).			
RL	[5]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF165).			
RP	MEDLINE=92231879; PubMed=1567395;			
RX	Weindel K., Marne D., Weich H.A.;			
RA	"AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor.";			
RT	Biochem. Biophys. Res. Commun. 183:1167-1174(1992).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM VEGF145).			
RX	MEDLINE=97207275; PubMed=9054410;			

34	94.5	11.9	204	1	PDGA_RAT	P28576 rattus norv
35	94.5	11.9	211	1	PDGA_MOUSE	P20033 mus musculus
36	94.5	11.9	213	1	PDGA_RABIT	P34007 oryctolagus
37	93	11.7	241	1	PDGB_MOUSE	P31240 mus musculus
38	92	11.6	225	1	PDGB_RAT	Q05028 rattus norv
39	89	11.2	28	1	ICPP_VIPLE	P82475 vipera lebe
40	81.5	10.3	2499	1	MPRI_BOVIN	P08169 bos taurus
41	80	10.1	799	1	ITBN_DRONE	Q27591 drosophila
42	74.5	9.4	471	1	MM13_RABIT	O62806 oryctolagus
43	74	9.3	354	1	VANA_PSESP	O05616 pseudomona
44	74	9.3	466	1	MM13_RAT	P23097 rattus norv
45	73	9.2	406	1	YMX2_CAEEL	P34510 caenorhabdi

## ALIGNMENTS

RA Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodaysky I.,  
 RA Keshet E., Neufeld G.;  
 RT "VEGF145, a secreted vascular endothelial growth factor isoform that  
 RT binds to extracellular matrix.";  
 RL J. Biol. Chem. 272:7151-7158(1997).  
 RN [7]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF183).  
 RC TISSUE-Kidney;  
 RX MEDLINE-99096474; PubMed-9878851;  
 RA Lei J., Jiang A., Pei D.;  
 RT "Identification and characterization of a new splicing variant of  
 RT vascular endothelial growth factor: VEGF183.";  
 RL Biochim. Biophys. Acta 1443:400-406(1998).  
 RN [8]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF165).  
 RP TISSUE-Breast;  
 RC MEDLINE-98119755; PubMed-9450968;  
 RA Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,  
 RA Abrams K.R., Lee S.W., Detmar M.;  
 RT "Identification of a human VPF/VEGF 3' untranslated region mediating  
 RT hypoxia-induced mRNA stability.";  
 RL Mol. Biol. Cell 9:469-481(1998).  
 RN [9]  
 RN SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).  
 RP TISSUE-Retina;  
 RC MEDLINE-99165303; PubMed-10067980;  
 RA Jingjing L., Xue Y., Agarwal N., Roque R.S.;  
 RT "Human Muller cells express VEGF183, a novel spliced variant of  
 RT vascular endothelial growth factor.";  
 RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).  
 RN [10]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF165).  
 RP TISSUE-Hemangioblastoma;  
 RC Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;  
 RA "Human cDNA for the vascular endothelial growth factor isoform  
 RT VEGF165.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF148).  
 RP TISSUE-Renal glomerulus;  
 RC MEDLINE-99394945; PubMed-10464055;  
 RA Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,  
 RA Harper S.J.;  
 RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA  
 RT and receptor mRNA expression in human glomeruli, and the  
 RT identification of VEGF148 mRNA, a novel truncated splice variant.";  
 RL Clin. Sci. 97:303-312(1999).  
 RN [12]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF121).  
 RP Sato J.D., Whitney R.G.;  
 RA "Human cDNA for vascular endothelial growth factor isoform VEGF121.";  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RN SEQUENCE FROM N.A.  
 RA Williams S.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RN SEQUENCE OF 23-232 FROM N.A. (VEGF165).  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RN PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.  
 RX MEDLINE-99062112; PubMed-2584205;  
 RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,  
 RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;  
 RT "Human vascular permeability factor. Isolation from U937 cells.";  
 RL J. Biol. Chem. 264:20017-20024(1989).  
 RN [16]  
 RN SEQUENCE OF 27-41.  
 RX MEDLINE-93145946; PubMed-7678805;  
 RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wiltling J.,  
 RA Kuchs G., Marne D., Hug H., Welch H.A.;

RT "Synthesis and assembly of functionally active human vascular  
 RT endothelial growth factor homodimers in insect cells.";  
 RL Eur. J. Biochem. 211:19-26(1993).  
 RN [17]  
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.  
 RX MEDLINE-97352774; PubMed-9207067;  
 RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,  
 RA de Vos A.M.;  
 RT "Vascular endothelial growth factor: crystal structure and functional  
 RT mapping of the kinase domain receptor binding site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).  
 RN [18]  
 RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.  
 RX MEDLINE-98035455; PubMed-9351807;  
 RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;  
 RT "The crystal structure of vascular endothelial growth factor (VEGF)  
 RT refined to 1.93-A resolution: multiple copy flexibility and receptor  
 RT binding.";  
 RL Structure 5:1325-1338(1997).  
 RN [19]  
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.  
 RX MEDLINE-99119204; PubMed-9922142;  
 RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,  
 RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;  
 RT "Crystal structure of the complex between VEGF and a receptor-blocking  
 RT peptide.";  
 RL Biochemistry 37:17765-17772(1998).  
 RN [20]  
 RN STRUCTURE BY NMR OF 34-135.  
 RX MEDLINE-97477915; PubMed-9336848;  
 RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
 RA Starovasnik M.A.;  
 RT "1H, 13C, and 15N backbone assignment and secondary structure of the  
 RT receptor-binding domain of vascular endothelial growth factor.";  
 RL Protein Sci. 6:2250-2260(1997).  
 RN [21]  
 RN STRUCTURE BY NMR OF 137-215.  
 RP MEDLINE-98298440; PubMed-9634701;  
 RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
 RA Starovasnik M.A.;  
 RT "Solution structure of the heparin-binding domain of vascular  
 RT endothelial growth factor.";  
 RL Structure 6:637-648(1998).  
 RN [22]  
 RN FUNCTION.  
 RP MEDLINE-21320570; PubMed-11427521;  
 RA Murphy J.F., Fitzgerald D.J.;  
 RT "Vascular endothelial growth factor induces cyclooxygenase-dependent  
 RT proliferation of endothelial cells via the VEGF-2 receptor.";  
 RL FASEB J. 15:1667-1669(2001).  
 CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PlGF (By similarity).  
 CC -1- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.  
 CC VEGF165 is more basic, has heparin-binding properties and,  
 CC although a significant proportion remains cell-associated, most is  
 CC freely secreted. VEGF189 is very basic; it is cell-associated  
 CC after secretion and is bound avidly by heparin and the  
 CC extracellular matrix, although it may be released as a soluble  
 CC form by heparin, heparinase or plasmin.  
 CC -1- ALTERNATIVE PRODUCTS: 7 isoforms: VEGF206 (shown here), VEGF189,  
 CC VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms  
 CC are widely expressed, whereas the VEGF206 and VEGF-145 are  
 CC uncommon.  
 CC -1- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,  
 CC nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.



```
Query Match      100.0%; Score 792; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60
DB 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60

QY 61 IFQEPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMIMRIKPHQGHIGEM 120
DB 61 IFQEPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMIMRIKPHQGHIGEM 120

QY 121 SFLQHNKCECRPKKDRARQEK 141
DB 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 2
VEGA_PIG
ID VEGA_PIG STANDARD; PRT; 190 AA.
AC P49151; Q9GL52;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95143284; PubMed=7841203;
RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT "Nucleotide sequence and expression of the porcine vascular
RT endothelial growth factor.";
RL Biochim. Biophys. Acta 1260:235-238(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee T., Canty J.M.;
RT "PCR cloning of porcine cardiac vascular endothelial growth factor
RT gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with p1GF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X81380; CAA57143.1; -
CC EMBL; AF318502; AAG33064.1; -
CC HSSP; P15692; 1VGH.
CC InterPro; IPR000072; PD_growth_factor.
CC Pfam; PF00341; PDGF; 1.
CC ProDom; PD001629; PD_growth_factor; 1.
```

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DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 190
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT DISULFID 100 100
FT CARBOHYD 102 102
FT CONFLICT T -> A (IN REF. 2).
SQ SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;

Query Match      92.6%; Score 733.5; DB 1; Length 190;
Best Local Similarity 95.7%; Pred. No. 5.6e-70;
Matches 134; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60
DB 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 59

QY 61 IFQEPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMIMRIKPHQGHIGEM 120
DB 61 IFQEPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMIMRIKPHQGHIGEM 119

QY 121 SFLQHNKCECRPKKDRARQEK 140
DB 121 SFLQHNKCECRPKKDRARQEK 139

RESULT 3
VEGA_CANFA
ID VEGA_CANFA STANDARD; PRT; 214 AA.
AC Q9MYV3; Q9XSF5; Q9XSF4; Q9XSF3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM VEGF188).
RX MEDLINE=20125516; PubMed=10661874;
RA Scheidegger P., Weighhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
RA Ballmer-Hofer K., Jaussel R.;
RT "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
RT bearing dogs.";
RL Biol. Chem. 380:1449-1454(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF188; VEGF-182 AND VEGF-164).
RC TISSUE=Heart;
RA Jingjing L., Roque R.S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with p1GF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; VEGF188 (shown here),
CC VEGF182 and VEGF164; are produced by alternative splicing.
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CC CC -----
CC CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: AJ133758; CAB82426.1; -
CC CC EMBL: AF133250; RAD29684.1; -
CC CC EMBL: AF133249; RAD29683.1; -
CC CC EMBL: AF133248; RAD29682.1; -
CC CC HSSP: P15692; 1VGP.
CC CC -----
CC CC InterPro: IPR000072; PD_growth_factor.
CC CC ProDom: PD001629; PD_growth_factor; 1.
CC CC SMART: SM00141; PDGF_1; 1.
CC CC PROSITE: PS00249; PDGF_1; 1.
CC CC PROSITE: PS0278; PDGF_2; 1.
CC CC Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
CC CC Heparin-binding; Alternative splicing; Multigene family.
CC CC POTENTIAL.
CC CC SIGNAL 1 26
CC CC CHAIN 27 214
CC CC DISULFID 51 93
CC CC DISULFID 82 127
CC CC DISULFID 86 129
CC CC DISULFID 76 76
CC CC DISULFID 85 85
CC CC CARBOHYD 100 100
CC CC VARSPLIC 140 140
CC CC VARSPLIC 141 164
CC CC VARSPLIC 159 164
CC CC CONFLICT 143 143
CC CC CONFLICT 161 161
CC CC SEQUENCE 214 AA; 25175 MW; 0AC980A158C44B27 CRC64;
CC CC -----
CC CC VASCULAR ENDOTHELIAL GROWTH FACTOR A.
CC CC BY SIMILARITY.
CC CC DISULFID 51 93
CC CC DISULFID 82 127
CC CC DISULFID 86 129
CC CC DISULFID 76 76
CC CC DISULFID 85 85
CC CC CARBOHYD 100 100
CC CC VARSPLIC 140 140
CC CC VARSPLIC 141 164
CC CC VARSPLIC 159 164
CC CC CONFLICT 143 143
CC CC CONFLICT 161 161
CC CC SEQUENCE 214 AA; 25175 MW; 0AC980A158C44B27 CRC64;
CC CC -----
CC CC Query Match 92.0%; Score 728.5; DB 1; Length 214;
CC CC Best Local Similarity 94.3%; Pred. No. 2.1e-69;
CC CC Matches 133; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
CC CC -----
CC CC QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60
CC CC DB 1 MNFLSWVHWSLALLYLHAKWSQAAPMA-GGEHKPHEVVKFMDVYQSYCHPIETLVD 59
CC CC QY 61 IFQEYDPEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMIMRIKPHOGQHIGEM 120
CC CC DB 60 IFQEYDPEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMIMRIKPHOGQHIGEM 119
CC CC QY 121 SFLQHNKCECRPKKDRARQEK 141
CC CC DB 120 SFLQHNKCECRPKKDRARQEK 140
CC CC -----
CC CC RESULT 4
CC CC VEGA_SHEEP STANDARD; PRT; 146 AA.
CC CC AC P50412;
CC CC DT 01-OCT-1996 (Rel. 34, Created)
CC CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC CC DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
CC CC permeability factor) (VPF).
CC CC GN VEGF OR VEGFA.
CC CC OS Ovis aries (Sheep).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC CC OC Bovidae; Caprinae; Ovis.
CC CC OX NCBI_TaxID=9940;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC TISSUE-Kidney;

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RX MEDLINE-97117958; PubMed-8958842;
RA Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
RA Reynolds L.P., Moor R.M.;
RT "Characterization and expression of vascular endothelial growth
RT factor (VEGF) in the ovine corpus luteum.";
RL J. Reprod. Fertil. 108:157-165(1996).
CC CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC CC endothelial cell growth. It induces endothelial cell
CC CC proliferation, promotes cell migration, inhibits apoptosis, and
CC CC induces permeabilization of blood vessels. It binds to the
CC CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC CC heparin (by similarity).
CC CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC CC with p1GF (by similarity).
CC CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: X89506; CAA61677.1; -
CC CC HSSP: P15692; 1VGP.
CC CC InterPro: IPR000072; PD_growth_factor.
CC CC Pfam: PF00341; PDGF_1; 1.
CC CC ProDom: PD001629; PD_growth_factor; 1.
CC CC SMART: SM00141; PDGF_1; 1.
CC CC PROSITE: PS00249; PDGF_1; 1.
CC CC PROSITE: PS0278; PDGF_2; 1.
CC CC Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
CC CC Heparin-binding; Multigene family.
CC CC SIGNAL 1 26
CC CC CHAIN 27 146
CC CC DISULFID 51 93
CC CC DISULFID 82 127
CC CC DISULFID 86 129
CC CC DISULFID 76 76
CC CC DISULFID 85 85
CC CC CARBOHYD 100 100
CC CC SEQUENCE 146 AA; 17247 MW; 4E792CB557F91760 CRC64;
CC CC -----
CC CC Query Match 90.8%; Score 719.5; DB 1; Length 146;
CC CC Best Local Similarity 92.2%; Pred. No. 1.2e-68;
CC CC Matches 130; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
CC CC -----
CC CC QY 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60
CC CC DB 1 MNFLSWVHWSLALLYLHAKWSQAAPMAE-GGOKPHEVVKFMDVYQSYCHPIETLVD 59
CC CC QY 61 IFQEYDPEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMIMRIKPHOGQHIGEM 120
CC CC DB 60 IFQEYDPEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMIMRIKPHOGQHIGEM 119
CC CC QY 121 SFLQHNKCECRPKKDRARQEK 141
CC CC DB 120 SFLQHNKCECRPKKDRARQEK 140
CC CC -----
CC CC RESULT 5
CC CC VEGA_BOVIN STANDARD; PRT; 190 AA.
CC CC AC P15691;
CC CC DT 01-APR-1990 (Rel. 14, Created)
CC CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC CC DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
CC CC permeability factor) (VPF).
CC CC GN VEGF OR VEGFA.
CC CC OS Bos taurus (Bovine).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OX Bovidae; Bovinae; Bos.  
 RN [1] NCBI\_TaxID=9913;  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.  
 RX MEDLINE=90069608; PubMed=2479986;  
 RA Leung D.W., Cachlanes G., Kuang W.-J., Goeddel D.V., Ferrara N.;  
 RT "Vascular endothelial growth factor is a secreted angiogenic  
 RT mitogen.";  
 RL Science 246:1306-1309(1989).  
 RN [2]  
 RP SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=90121225; PubMed=2610687;  
 RA Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,  
 RA Lau K., Crisp T., Fiddes J.C., Abraham J.A.;  
 RT "Vascular endothelial growth factor: a new member of the platelet-  
 RT derived growth factor gene family.";  
 RL Biochem. Biophys. Res. Commun. 165:1198-1206(1989).  
 RN [3]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=89286596; PubMed=2735925;  
 RA Ferrara N., Henzel W.J.;  
 RT "pituitary follicular cells secrete a novel heparin-binding growth  
 RT factor specific for vascular endothelial cells.";  
 RL Biochem. Biophys. Res. Commun. 161:851-858(1989).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PLGF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
 CC to the extracellular matrix unless released by heparin (By  
 CC similarity).  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are  
 CC produced by alternative splicing.  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC -----  
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 CC -----  
 CC EMBL; M32976; AAA30502.1; -;  
 CC EMBL; M31836; AAA30804.1; -;  
 CC EMBL; M33750; AAA30805.1; -;  
 CC PIR; A33255; A33255.  
 CC PIR; A33787; A33787.  
 CC PIR; B40080; B40080.  
 CC HSP; P15692; IVGH.  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS00278; PDGF\_2; 1.  
 CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;  
 KW Heparin-binding; Alternative splicing; Multigene family.  
 FT SIGNAL 1 26  
 FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
 FT DISULFID 51 93 BY SIMILARITY.  
 FT DISULFID 82 127 BY SIMILARITY.  
 FT DISULFID 86 129 BY SIMILARITY.  
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPLIC 139 183 MISSING (IN ISOFORM BETA).  
 FT VARSPLIC 184 184 R -> K (IN ISOFORM BETA).

SQ SEQUENCE 190 AA; 22310 MW; EDBF903E46E24789 CRC64;  
 Query Match 90.6%; Score 717.5; DB 1; Length 190;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-68;  
 Matches 130; Conservative 3; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 MNFLLSWVHSLALLYLHHAQKWSQAAPMAEGGQGNHHEVVKFMDVYQRSYCHPIETLVD 60  
 Db 1 MNFLLSWVHSLALLYLHHAQKWSQAAPMAE-GGQKPEVVKFMDVYQRSYCHPIETLVD 59  
 QY 61 IQEYYPDEIEYIFKPCVPLMRCGGCCNDEGLECYPTESNITMQIMRKPHQGHIGEM 120  
 Db 60 IQEYYPDEIEYIFKPCVPLMRCGGCCNDEGLECYPTESNITMQIMRKPHQGHIGEM 119  
 QY 121 SFLOHNKCECRPKDKARQOE 140  
 Db 120 SFLOHNKCECRPKDKARQOE 139  
 RESULT 6  
 VEGA\_HORSE  
 ID VEGA\_HORSE STANDARD; PRT; 190 AA.  
 AC Q9GKR0.  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular  
 DE permeability factor) (VPF).  
 GN VEGF OR VEGFA.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S.,  
 RA Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;  
 RT "Cloning of cDNA and high-level expression of equine vascular  
 RT endothelial growth factor (VEGF).";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth. Induces endothelial proliferation and vascular  
 CC permeability (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PLGF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
 CC to the extracellular matrix unless released by heparin (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC -----  
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 CC -----  
 CC EMBL; AB053350; BAB20890.1; -;  
 CC HSP; P15692; IVGH.  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS00278; PDGF\_2; 1.  
 CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
 FT DISULFID 51 93 BY SIMILARITY.  
 FT DISULFID 82 127 BY SIMILARITY.  
 FT DISULFID 86 129 BY SIMILARITY.

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FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 190 AA; 22312 MW; 87E9E161439E5F87 CRC64;

Query Match 89.5%; Score 708.5; DB 1; Length 190;
Best Local Similarity 92.1%; Pred. No. 2.4e-67;
Matches 129; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNFLLSWHWSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 60
DB 1 MNFLLSWHWSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHGEM 120
DB 60 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHGEM 119

QY 121 SFLQHNKCECRPKDRARQE 140
DB 120 SFLQHSKCECRPKDRARQE 139

RESULT 7
VEGA_MOUSE STANDARD; PRT; 214 AA.
AC Q00731;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
RX MEDLINE=92274860; PubMed=1592003;
RA Breier G., Albrecht U., Sterrer S., Risau W.;
RT "Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation.";
RL Development 114:521-532(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-1).
RX MEDLINE=92355593; PubMed=1644816;
RA Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT "Vascular endothelial growth factor. Regulation by cell differentiation and activated second messenger pathways.";
RL J. Biol. Chem. 267:16317-16322(1992).
RN [3]
RP SEQUENCE OF 1-3 FROM N.A.
RX MEDLINE=96216498; PubMed=8632007;
RA Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
RT "The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and characterization of transcriptional and post-transcriptional regulatory sequences.";
RL J. Biol. Chem. 271:3877-3883(1996).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3 remains cell-surface associated unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; VEGF-3/VEGF188 (shown here), VEGF-1/VEGF164 and VEGF-2/VEGF120; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the choroid plexus, paraventricular neuroepithelium, placenta and kidney glomeruli. Also found in bronchial epithelium, adrenal gland and in seminiferous tubules of testis. High expression of VEGF continues in kidney glomeruli and choroid plexus in adults.
-1- DOMAIN: VEGF-3 contains a basic insert which acts as a cell retention signal.
-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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EMBL; S37052; AAB22252.1; -
EMBL; S38083; AAB22253.1; -
EMBL; S38100; AAB22254.1; -
EMBL; M95200; AAA40547.1; -
EMBL; U41383; -; NOT_ANNOTATED_CDS.
PIR; A43351; A43351.
HSP; P15692; 2VPF.
MGD; MGI:103178; Vegfa.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 214 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (PROBABLE).
FT VARSPLIC 140 140 K -> N (IN ISOFORM VEGF-1).
FT VARSPLIC 141 164 MISSING (IN ISOFORM VEGF-1).
FT VARSPLIC 141 208 MISSING (IN ISOFORM VEGF-2).
FT CONFLICT 117 118 GE -> ER (IN REF. 2).
SQ SEQUENCE 214 AA; 25283 MW; B5540B51E4BB6E17 CRC64;

Query Match 86.7%; Score 686.5; DB 1; Length 214;
Best Local Similarity 87.2%; Pred. No. 5.5e-65;
Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSWHWSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 60
DB 1 MNFLLSWHWSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHGEM 120
DB 60 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHGEM 119

QY 121 SFLQHNKCECRPKDRARQE 141
DB 120 SFLQHSRCECRPKDRARQE 140

RESULT 8
VEGA_MOUSE STANDARD; PRT; 214 AA.
AC P16612; Q9QXG7; Q9QXG6; Q9JXY7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.

```

OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.  
 RX MEDLINE=90207249; PubMed=2320579;  
 RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,  
 RA Palisi T.M., Hope D.A., Thomas K.A.;  
 RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen  
 RT that is homologous to platelet-derived growth factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS VEGF-A188; VEGF-A164; VEGF-A144 AND  
 RP VEGF-A120).  
 RA Ishii H., Arakawa T., Okayama M., Oota I., Takuma T., Inomata K.;  
 RT "Developmental expression of vascular endothelial growth factor-A  
 RT (VEGF-A) splicing variants, VEGF-A188, VEGF-A164, and VEGF-A120 in rat  
 RT masseter muscle.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 27-40.  
 RC TISSUE=Glial tumor;  
 RX MEDLINE=95221439; PubMed=7706320;  
 RA DiSalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,  
 RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;  
 RT "Purification and characterization of a naturally occurring vascular  
 RT endothelial growth factor/placenta growth factor heterodimer.";  
 RL J. Biol. Chem. 270:7717-7723(1995).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with p1GF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted.  
 CC VEGF-A164 is more basic, has heparin-binding properties and,  
 CC although a significant proportion remains cell-associated, most is  
 CC freely secreted. VEGF-A188 is very basic; it is cell-associated  
 CC after secretion and is bound avidly by heparin and the  
 CC extracellular matrix, although it may be released as a soluble  
 CC form by heparin, heparinase or plasmin (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS: At least 4 isoforms: VEGF-A188 (shown here),  
 CC VEGF-A164, VEGF-A144 and VEGF-A120; are produced by alternative  
 CC splicing.  
 CC -!- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in  
 CC particularly in supraoptic and paraventricular nuclei and the  
 CC choroid plexus. Also found abundantly in the corpus luteum of  
 CC the ovary and in kidney glomeruli.  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M32167; AAA41211.1; -  
 CC DR EMBL; AF215725; AAF19211.1; -  
 CC DR EMBL; AF215726; AAF19212.1; -  
 CC DR EMBL; AF222779; AAF25958.1; -  
 CC DR PIR; A35987; A35987.  
 CC DR HSSP; P15692; 1VPP.  
 CC DR InterPro; IPR000072; PD\_growth\_factor.  
 CC DR Pfam; PF00341; PDGF; 1  
 CC DR ProDom; PD001629; PD\_growth\_factor; 1.  
 CC DR SMART; SM00141; PDGF; 1.  
 CC DR PROSITE; PS00249; PDGF\_1; 1.  
 CC DR PROSITE; PS0278; PDGF\_2; 1.

KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;  
 KW Heparin-binding; Alternative splicing; Multigene family.  
 FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
 FT CHAIN 27 214 BY SIMILARITY.  
 FT DISULFID 51 93 BY SIMILARITY.  
 FT DISULFID 82 127 BY SIMILARITY.  
 FT DISULFID 86 129 BY SIMILARITY.  
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC...).  
 FT VARSPLIC 140 140 K -> N (IN ISOFORM VEGF-A164).  
 FT VARSPLIC 141 164 MISSING (IN ISOFORM VEGF-A164).  
 FT VARSPLIC 141 208 MISSING (IN ISOFORM VEGF-A120).  
 FT VARSPLIC 165 208 MISSING (IN ISOFORM VEGF-A144).  
 FT CONFLICT 101 101 V -> A (IN REF. 2; AAF19212).  
 SQ SEQUENCE 214 AA; 25239 MW; 60FB8876F5304946 CRC64;  
 Query Match 86.6%; Score 685.5; DB 1; Length 214;  
 Best Local Similarity 87.2%; Pred. No. 7e-65;  
 Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;  
 QY 1 MNFLSNVWHSLSALLLYLHHAKWSQAAPKAEGGGQNHHEVYKFMVYORSYCHPIETLVD 60  
 Db 1 MNFLSNVWHSLSALLLYLHHAKWSQAAPTE-GEOKAHEVYKFMVYORSYCHPIETLVD 59  
 QY 61 FQOEYDIEYIFKPCVPLMRGCGCCNDGECVPTESNITMOIMRIKPHQGHIGEM 120  
 Db 60 FQOEYDIEYIFKPCVPLMRGCGCCNDGECVPTESNITMOIMRIKPHQGHIGEM 119  
 QY 121 SFLQNKCECRPKDRAQEK 141  
 Db 120 SFLQHSRCECRPKDRTKPEK 140  
 RESULT 9  
 ID VEGA\_MESAU STANDARD; PRG; 190 AA.  
 AC Q99PS1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular  
 DE permeability factor) (VPF).  
 GN VEGF OR VEGFA.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Decidua, and Embryo;  
 RA Yi X.J., Chow P.H.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with p1GF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
 CC to the extracellular matrix unless released by heparin (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M32167; AAA41211.1; -  
 CC DR EMBL; AF215725; AAF19211.1; -  
 CC DR EMBL; AF215726; AAF19212.1; -  
 CC DR EMBL; AF222779; AAF25958.1; -  
 CC DR PIR; A35987; A35987.  
 CC DR HSSP; P15692; 1VPP.  
 CC DR InterPro; IPR000072; PD\_growth\_factor.  
 CC DR Pfam; PF00341; PDGF; 1  
 CC DR ProDom; PD001629; PD\_growth\_factor; 1.  
 CC DR SMART; SM00141; PDGF; 1.  
 CC DR PROSITE; PS00249; PDGF\_1; 1.  
 CC DR PROSITE; PS0278; PDGF\_2; 1.

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CC  EMBL; AF063013; AAK00049.1; -
CC  HSSP; P15692; 1VGH.
DR  InterPro; IPR000072; PD_growth_factor.
DR  Pfam; PF00341; PDGF; 1.
DR  ProDom; PD001629; PD_growth_factor; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS00249; PDGF_1; 1.
DR  PROSITE; PS02078; PDGF_2; 1.
KW  Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW  Heparin-binding; Multigene family.
FT  SIGNAL 1 26
FT  CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT  DISULFID 51 93
FT  DISULFID 82 127
FT  DISULFID 86 129
FT  DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT  DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 190 AA; 22276 MW; F00C5A8EA79A465F CRC64;

Query Match 84.0%; Score 665.5; DB 1; Length 190;
Best Local Similarity 85.0%; Pred. No. 7.7e-63;
Matches 119; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59
Qy 61 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLCVPTESNITMQIMRKPHQSQHIGEM 120
Db 60 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLCVPTESNITMQIMRKPHQSQHIGEM 119
Qy 121 SFLOHNKCECRPKKDRARQE 140
Db 120 SFLOHRCRCRPPKVRKPE 139

RESULT 10
VEGA_CHICK STANDARD; PRT; 216 AA.
AC P52582; Q91420;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VFP).
GN VEGF OR VEGFA.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Chicken; TISSUE=Heart;
RA Takahashi T.;
RT "Chick embryonic ventricular myocytes VEGF.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.c.japonica; TISSUE=Embryo;
RA Flame I., von Reuten M., Drexler H.C., Syed-Ali S., Risau W.;
RT "Overexpression of vascular endothelial growth factor in the avian
RT embryo induces hypervascularization and increased vascular
RT permeability without alterations of embryonic pattern formation.";
RL Dev. Biol. 171:399-414(1995).
RN [3]
RP SEQUENCE OF 60-187 FROM N.A.
RC SPECIES=C.c.japonica;

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RX MEDLINE-95301109; PubMed-7781909;
RA Flame I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT (f1k-1) are expressed during vasculogenesis and vascular
RT differentiation in the quail embryo.";
RL Dev. Biol. 169:699-712(1995).
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; VEGF190 (shown here),
CC VEGF166 and VEGF146; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Abundantly and equally expressed in heart and
CC liver. In kidney glomeruli, brain and yolk sac, VEGF166 is 5- to
CC 10-times more abundant than VEGF190.
CC -!- DEVELOPMENTAL STAGE: VEGF166 is expressed early at day 1 and is
CC upregulated during gastrulation. Expression of VEGF190 is detectable
CC only from day 2.
CC -!- DOMAIN: VEGF190 contains a basic insert which acts as a cell
CC retention signal.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB011078; BAA24925.1; -
DR EMBL; S79680; AAB35371.1; -
DR HSSP; P15692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS02078; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 216 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT DISULFID 86 86 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 142 142 K -> N (IN ISOFORM VEGF-166).
FT VARSPLIC 143 166 MISSING (IN ISOFORM VEGF-146).
FT VARSPLIC 166 166 F -> L (IN ISOFORM VEGF-146).
FT VARSPLIC 167 210 MISSING (IN ISOFORM VEGF-146).
SQ SEQUENCE 216 AA; 25203 MW; 82E669C2F6FC6DA7 CRC64;

Query Match 70.1%; Score 555.5; DB 1; Length 216;
Best Local Similarity 68.3%; Pred. No. 3.2e-51;
Matches 97; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Qy 61 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLCVPTESNITMQIMRKPHQSQHIGEM 120
Db 60 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLCVPTESNITMQIMRKPHQSQHIGEM 120
Qy 121 SFLOHNKCECRPKKDRARQE 141
Db 120 SFLOHRCRCRPPKVRKPE 139

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Db 121 SPLQHSKDCRPPKDVKNKQEK 142
VEGA_CAVPO STANDARD; PRT; 164 AA.
RESULT 11
AC P26617;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
factor) (VPF).
GN VEGF OR VEGFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blle duct;
RA Berse B.;
RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
cell growth. Induces endothelial proliferation and vascular
permeability (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
with PLGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
to the extracellular matrix unless released by heparin (By
similarity).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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or send an email to license@isb-sib.ch).
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EMBL; M84230; AAA37057.1; -
HSP; P15692; LVGH.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS02278; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein.
FT DISULFID 25 67 BY SIMILARITY.
FT DISULFID 56 101 BY SIMILARITY.
FT DISULFID 60 103 BY SIMILARITY.
FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT DISULFID 59 59 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 164 AA; 19330 MW; 9EB6A81A9D5DCA4 CRC64;
Query Match 68.6%; Score 543.5; DB 1; Length 164;
Best Local Similarity 87.7%; Pred. No. 4.2e-50;
Matches 100; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
QY 27 APMAEGGQNHVEVVKFMDVYQSYCHPIETLVDFQEPDEIEYIFKPSVPLMRCGCGC 86
||||| 1 | |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APMAE-GEQKPREEVKMDVYKSYCRPIELMDVDFQEPDEIEYIFKPSVPLMRCGCGC 59
QY 87 CNDEGLECVPTESNITMQIMRIKPHQGHIGMSFLQHNKCECRPKKDRARQE 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 CNDESLECVPTFEENITMQIMRIKPHQGHIGMSFLQHSKCECRPKKKEARQE 113
RESULT 12
PLGF_BOVIN
ID PLGF_BOVIN STANDARD; PRT; 149 AA.
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AC Q9XS47;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Placenta growth factor precursor (PIGF).
GN PGF OR PLGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RL "Structure and expression of bovine VEGF family.";
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial
cell growth, stimulating their proliferation and migration. It
binds to receptor VEGFR-1/Flt1 (By similarity).
CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
heterodimer with VEGF/VEGF-A (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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EMBL; AB004272; BAA77684.1; -
HSP; P49763; LFZV.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS02278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal.
FT CHAIN 1 18 POTENTIAL.
FT SIGNAL 19 149 PLACENTA GROWTH FACTOR.
FT DISULFID 52 94 INTRACHAIN (BY SIMILARITY).
FT DISULFID 83 128 INTRACHAIN (BY SIMILARITY).
FT DISULFID 87 130 INTRACHAIN (BY SIMILARITY).
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT DISULFID 86 86 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 149 AA; 17094 MW; 1F8EE3BBC745EFE0 CRC64;
Query Match 40.4%; Score 320; DB 1; Length 149;
Best Local Similarity 46.7%; Pred. No. 1.le-26;
Matches 56; Conservative 23; Mismatches 37; Indels 4; Gaps 1;
QY 22 KWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVDFQEPDEIEYIFKPSVPLM 81
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 26 QMA----LSPGNISSEVEVPFQQWSRSYCRPVERLVDIVSEYSEMHUFLFSPSCVSLM 81
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 RCGGCNDGEGLECVPTESNITMQIMRIKPHQGHIGMSFLQHNKCECRPKKDRARQE 141
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 RCTGCCSDSMHCVPLETANVTMQLMKYRSLDQPFVEMSFQHVRCCKPLWEKMKQTR 141
RESULT 13
PLGF_MOUSE
ID PLGF_MOUSE STANDARD; PRT; 158 AA.
AC P49764;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```





RA Tucci M., Persico M.G., Acharya K.R.;  
 RT "the crystal structure of human placenta growth factor-1 (PLGF-1), an  
 RL angiogenic protein, at 2.0 Å resolution.";  
 CC J. Biol. Chem. 276:12153-12161(2001).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth, stimulating their proliferation and migration. It  
 CC binds to receptor VEGFR-1/Flt1. PLGF-2 binds neuropilin-1 and 2 in  
 CC a heparin-dependent manner.  
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as  
 CC heterodimer with VEGF/VEGF-A. PLGF-3 is found both as homodimer  
 CC and as monomer.  
 CC -!- SUBCELLULAR LOCATION: The three forms are secreted but PLGF-2  
 CC appears to remain cell attached unless released by heparin.  
 CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; PLGF-1/PLGF-131, PLGF-2/PLGF-152  
 CC and PLGF-3 (shown here); are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: While the three forms are present in most  
 CC placental tissues, the PLGF-2 is specific to early (8 week)  
 CC placenta and only PLGF-1 is found in the colon and mammary  
 CC carcinomas.  
 CC -!- DOMAIN: PLGF-2 contains a basic insert which acts as a cell  
 CC retention signal.  
 CC -!- PTM: N-GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X54936; CAA38698.1; -;  
 CC EMBL; S72960; AAB30462.2; -;  
 CC EMBL; S57152; AAB25832.2; ALT\_SEQ.  
 CC EMBL; AC006530; AAD30179.1; -;  
 CC EMBL; BC001422; AA01422.1; -;  
 CC EMBL; BC007789; AA07789.1; -;  
 CC EMBL; BC007255; AA07255.1; -;  
 CC EMBL; AL8411; CAA01393.1; -;  
 CC DB: JF2V; 09-MAY-01.  
 CC Genew: HGNC:8893; PGF.  
 CC MIM: 601121; -;  
 CC InterPro: IPR000072; PD\_growth\_factor.  
 CC Pfam: PF00341; PDGF; 1.  
 CC ProDom: PD001629; PD\_growth\_factor; 1.  
 CC SMART: SM00141; PDGF; 1.  
 CC PROSITE: PS00249; PDGF\_1; 1.  
 CC PROSITE: PS0278; PDGF\_2; 1.  
 CC Mitogen: Growth factor; Glycoprotein; Signal; Heparin-binding;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 18  
 FT CHAIN 19 221 PLACENTA GROWTH FACTOR.  
 FT DOMAIN 193 213 HEPARIN-BINDING (PROBABLE).  
 FT DISULFID 52 94  
 FT DISULFID 83 128  
 FT DISULFID 87 130  
 FT DISULFID 77 77 INTERCHAIN.  
 FT DISULFID 86 86 INTERCHAIN.  
 FT DISULFID 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 132 203 MISSING (IN ISOFORM PLGF-1 AND ISOFORM  
 FT PLGF-2).  
 FT VARSPLIC 213 213 R -> RRRPKGRKRRRQRPTDCHL (IN ISOFORM  
 FT PLGF-2).  
 FT CONFLICT 91 91 N -> D (IN REF. 2).  
 SQ SEQUENCE 221 AA; 24788 MW; D364C6A73C1C6987 CRC64;  
 Query Match 38.9%; Score 308; DB 1; Length 221;  
 Best Local Similarity 47.0%; Pred. No. 3.2e-25;  
 Matches 54; Conservative 21; Mismatches 36; Indels 4; Gaps 1;

Db 26 QWALSA-----GNGSEVEVPFQEWGRSYCRALERLVDVYSEYSEVHMFSPSCVSL 81  
 Qy 82 RCGCCNDGEGECYPTESNTMTQIMRIKPHQGHIGEMSFLOHKNKCRPKDR 136  
 Db 82 RTGCGGDNLHCPVETANVTMQLLKIRSGDRPSYVELTFSQHVRCRHSR 136  
 RESULT 15  
 PGLE\_RAT PGLE\_RAT STANDARD; PRT; 158 AA.  
 ID AC Q63434;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Placenta growth factor precursor (PIGF).  
 GN PIGF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=95221439; PubMed=7706320;  
 RA Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,  
 RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;  
 RT "Purification and characterization of a naturally occurring vascular  
 RT endothelial growth factor/placenta growth factor heterodimer.";  
 RL J. Biol. Chem. 270:7717-7723(1995).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth, stimulating their proliferation and migration. It  
 CC binds to receptor VEGFR-1/Flt1 (by similarity).  
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as  
 CC heterodimer with VEGF/VEGF-A.  
 CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L40030; AAA97426.1; -;  
 CC HSSP; P49763; IF2V.  
 CC InterPro: IPR000072; PD\_growth\_factor.  
 CC Pfam: PF00341; PDGF; 1.  
 CC ProDom: PD001629; PD\_growth\_factor; 1.  
 CC SMART: SM00141; PDGF; 1.  
 CC PROSITE: PS00249; PDGF\_1; 1.  
 CC PROSITE: PS0278; PDGF\_2; 1.  
 CC Mitogen: Growth factor; Glycoprotein; Signal.  
 KW SIGNAL 1 23  
 FT CHAIN 24 158 PLACENTA GROWTH FACTOR.  
 FT DISULFID 48 90 INTRACHAIN (BY SIMILARITY).  
 FT DISULFID 79 125 INTRACHAIN (BY SIMILARITY).  
 FT DISULFID -83 127 INTRACHAIN (BY SIMILARITY).  
 FT DISULFID 73 73 INTRACHAIN (BY SIMILARITY).  
 FT DISULFID 82 82 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 158 AA; 17681 MW; B4771373A82E15B9 CRC64;  
 Query Match 37.1%; Score 294; DB 1; Length 158;  
 Best Local Similarity 48.7%; Pred. No. 6.5e-24;  
 Matches 58; Conservative 19; Mismatches 40; Indels 2; Gaps 2;

Qy 24 SQAAPMAGCGGNHHEVVKFMDVYQSRYPCHP1ETLVDFQYDEIEYFIPKPCVPLMRC 83  
 Db 21 SQGA-LSAGNNSTEMEVVYFFNEVGRSGRCPMEKLVYIADEHPNEVSHFSPSCVLLSRC 79

Qy 84 GGCNDEGLECVPTESNITMIMRIKPHQGH-IGEMSFLOHNKCECRPKKDRARQEK 141  
Db 80 SGGCGDEGLHCVALKTANITMILKIPNRPDHPHSYVENTFSQDVLCRCRPILETTKAER 138

Search completed: November 20, 2002, 04:57:29  
Job time : 39 secs

Result No.	Query	Score	8			Description
			Match	Length	ID	
1	787	99.4	191	4	Q96L82	
2	787	99.4	191	4	Q96K10	
3	787	99.4	191	6	Q95NE5	
4	714.5	90.2	190	6	Q77643	
5	708.5	89.5	189	6	Q95D47	
6	703	88.8	126	6	Q98DP7	
7	695.5	87.8	190	11	Q90X39	
8	680.5	85.9	190	11	Q91ZE1	
9	575.5	72.7	124	6	Q8SP29	
10	561.5	70.9	118	6	Q9MZB1	
11	555	70.1	124	6	Q9GK00	
12	536.5	67.7	148	13	Q42571	
13	536	67.7	128	6	Q8SP15	
14	532	67.2	127	6	Q9WMQ4	
15	531.5	67.1	194	13	Q42572	
16	510.5	64.5	141	11	O70123	

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|||||
Db 121 SFLQHNKCECRPKKDRARQE 140

RESULT 2
Q96KJ0
ID Q96KJ0 PRELIMINARY; PRT; 191 AA.
AC Q96KJ0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor 165b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Sugiono M., Winkler M., Gillatt D., Harper S.J., Bates D.O.;
RT "A new isoform of vascular endothelial growth factor mRNA is down-
regulated in renal tumors.";
RL (In) Unknown A. (eds.);
RL Proceedings of the 7th World Congress on Microcirculation, pp.3-3,
RL Sydney, Australia (2001).
DR EMBL; AF430806; AAL27435.1; -.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 191 AA; 2258 MW; D25243E540AC79BD CRC64;

Query Match 99.4%; Score 787; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 120
Db 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
Db 121 SFLQHNKCECRPKKDRARQE 140
|||||

RESULT 3
Q95NE5
ID Q95NE5 PRELIMINARY; PRT; 191 AA.
AC Q95NE5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SimVEGF165.
GN SIMVEGF165.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96245208; PubMed=8641836;
RA Shima D.T., Gougos A., Miller J.W., Tolentino M., Robinson G.,
RA Adams A.P., D'Amore P.A.;
RT "Cloning and mRNA expression of vascular endothelial growth factor in
ischemic retinas of Macaca fascicularis.";
RL Invest. Ophthalmol. Vis. Sci. 37:1334-1340(1996).
DR EMBL; S82167; AAB47118.1; -.

Query Match 99.4%; Score 787; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 120
Db 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
Db 121 SFLQHNKCECRPKKDRARQE 140
|||||

RESULT 4
Q77643
ID Q77643 PRELIMINARY; PRT; 190 AA.
AC Q77643;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA-RAMBOULLIET;
RA Cheung C.Y., Brace R.A.;
RT "Ovine vascular endothelial growth factor: Nucleotide sequence and
expression in fetal tissues.";
RL Growth Factors 0:0-0(1998).
DR EMBL; AF071015; AAC23608.1; -.
DR HSP; P15692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22342 MW; 0D5E3B3E5C53E739 CRC64;

Query Match 90.2%; Score 714.5; DB 6; Length 190;
Best Local Similarity 92.1%; Pred. No. 3.9e-72;
Matches 129; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAE-GGQKPEVVKFMDVYQSYCHPIETLVD 59
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 120
Db 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLCECVPTESNITMQIMRIKPHOGHIGEM 119
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
Db 120 SFLQHNKCECRPKKDRARQE 139
|||||

RESULT 5
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Q95LQ4
ID Q95LQ4; PRELIMINARY; PRT; 189 AA.
AC Q95LQ4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Koga L., Kobayashi Y., Yazawa M., Masuda K., Ohno K., Tsujimoto H.;
RT "Nucleotide sequence and expression of the feline vascular endothelial
RT growth factor.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071947; BAB68520.1; -.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 189 AA; 22193 MW; C1E4646759AB3FD6 CRC64;

Query Match 89.5%; Score 708.5; DB 6; Length 189;
Best Local Similarity 92.1%; Pred. No. 1.8e-71;
Matches 128; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLLSWHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLLSWHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 120
Db 60 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 119
QY 121 SFLOHNSKCECRPKKDRARQ 139
Db 120 SFLOHNSKCECRPKKDRAKE 138

RESULT 6
Q9BDP7
ID Q9BDP7; PRELIMINARY; PRT; 126 AA.
AC Q9BDP7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hazzard T.M., Navak N.R., Jia Y., Stouffer R.L.;
RT "Rhesus macaque VEGF mRNA sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF339737; AAK26379.1; -.
DR HSSP; PI5692; 2VPF.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14599 MW; 1175F2386A883BCF CRC64;

Query Match 88.8%; Score 703; DB 6; Length 126;

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Best Local Similarity 99.2%; Pred. No. 4.8e-71;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYPD 67
Db 1 VHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYPD 60
QY 68 EIEYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEMSFLQHNK 127
Db 61 EIEYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEMSFLQHNK 120
QY 128 CECRPK 133
Db 121 CECRPK 126

RESULT 7
Q9QX39
ID Q9QX39; PRELIMINARY; PRT; 190 AA.
AC Q9QX39;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
OS VEGF.
OC Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP SEQUENCE FROM N.A.
RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;
RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax
RT ehrenbergi: the role of vascular endothelial growth factor.";
RL FEBS Lett. 452:133-140(1999).
DR EMBL; AF186236; AAD56245.1; -.
DR HSSP; PI5692; 2VPF.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22488 MW; 2228383BC5F0BFE CRC64;

Query Match 87.8%; Score 695.5; DB 11; Length 190;
Best Local Similarity 89.3%; Pred. No. 5.2e-70;
Matches 125; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MNFLLSWHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLLSWHSVLSALLYLHHAKWSQAAPNAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 120
Db 60 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 119
QY 121 SFLOHNSKCECRPKKDRARQ 140
Db 120 SFLOHNSKCECRPKKDRTRLE 139

RESULT 8
Q91ZE1
ID Q91ZE1; PRELIMINARY; PRT; 190 AA.
AC Q91ZE1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
OS VEGF.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Marion S., Lee T.-C.;
RT "Cloning of multiple VEGF splice variants from hypoxic neonatal rat
cardiomyocytes.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033506; AAL07526.1; -.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR ProSITE; PS00249; PDGF_1; UNKNOWN_1.
DR ProSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22396 MW; 589374010441F377 CRC64;

Query Match 85.9%; Score 680.5; DB 11; Length 190;
Best Local Similarity 87.1%; Pred. No. 2.5e-68;
Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSNVHSLALLLHLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
D 1 MNFLLSNVHSLALLLHLHAKWSQAAPTE-GEQKAHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQSHIGEM 120
D 60 IFQYEPDEIEYIFKPCVPLMRCAGCCNDEALECVPTESNITMQIMRIKPHQSHIGEM 119
QY 121 SFLOHNCCEPRKKDRARQE 140
D 120 SFLOHRCCEPRKKDRKPE 139

RESULT 9
Q8SP29 ID Q8SP29 PRELIMINARY; PRT; 124 AA.
AC Q8SP29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYOCARDIUM;
RA Yuan H., Li J.;
RT "The expression of VEGF in porcine collateral-dependent myocardial by
exercise training.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461807; AAL85286.1; -.
DR ProDom: 124 124
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 14552 MW; 2E1C1A009E67C9C9 CRC64;

Query Match 72.7%; Score 575.5; DB 6; Length 124;
Best Local Similarity 94.6%; Pred. No. 9.1e-57;
Matches 106; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 29 MAEGGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPCVPLMRCGCCN 88
D 1 MAE-GDQKPEHVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPCVPLMRCGCCN 59
QY 89 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 141
D 60 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 112

RESULT 10
Q8SP29 ID Q8SP29 PRELIMINARY; PRT; 124 AA.
AC Q8SP29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVIDUCT;
RA Welter H., Gabler C., Einspanier R.;
RT "growth factor expression in marmoset monkey oviducts.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278192; CAC19523.1; -.
DR HSSP; P15692; IVGH.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR ProSITE; PS00249; PDGF_1; 1.
DR ProSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 1
FT NON_TER 124 124
```

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Q9MZB1 ID Q9MZB1 PRELIMINARY; PRT; 118 AA.
AC Q9MZB1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTAL ARTERY ENDOTHELIUM;
RA Zheng J., Tsai S.C., Magnus R.R.;
RT "Growth factor expression in ovine fetal placental artery endothelial
cells.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250375; AAF75258.1; -.
DR HSSP; P15692; IVPP.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR ProSITE; PS00249; PDGF_1; 1.
DR ProSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13931 MW; 757DC59AA56378A6 CRC64;

Query Match 70.9%; Score 561.5; DB 6; Length 118;
Best Local Similarity 90.3%; Pred. No. 3.2e-55;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 29 MAEGGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPCVPLMRCGCCN 88
D 1 MAE-GGQKPEHVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPCVPLMRCGCCN 59
QY 89 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 141
D 60 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 112

RESULT 11
Q9GK00 ID Q9GK00 PRELIMINARY; PRT; 124 AA.
AC Q9GK00;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVIDUCT;
RA Welter H., Gabler C., Einspanier R.;
RT "growth factor expression in marmoset monkey oviducts.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278192; CAC19523.1; -.
DR HSSP; P15692; IVGH.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR ProSITE; PS00249; PDGF_1; 1.
DR ProSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 1
FT NON_TER 124 124
```

Equus caballus (horse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

```
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Vascular endothelial growth factor 196.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT "Neovascularization of the Xenopus embryo.";
RL Dev. Dyn. 0:0-0(1997).
DR EMBL; AF008594; AAB63680.1; -.
DR HSSP; P15692; LVGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 194 AA; 22672 MW; 85D7BEC7CEFEF17E CRC64;

Query Match      67.1%; Score 531.5; DB 13; Length 194;
Best Local Similarity 69.5%; Pred. No. 1.3e-51;
Matches 98; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 1 MNFLLSVHVHSLALLLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVD 60
Db 1 MNFLPWIHWGLAVLLYIPHAQLSGRAPMGEGDHPTEVVKFKVYERSMCQVRELLVD 60

QY 61 IFQEYDEIEYIFKPSCVPLMRGCGCNDGECVPTESNITMQIMRIKPHQGQHIGEM 120
Db 61 IFQEYDEVEYIFKPSCVPLMRGCGCNDGECVPTESNITMQIMRIKPHISQHIMDM 120

QY 121 SFLQHNKCECRPKD-RAROE 140
Db 121 SFOQHSQCECRPKRKEVKSKE 141
```

Search completed: November 20, 2002, 04:59:26  
Job time : 95 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 04:58:43 ; Search time 273 Seconds  
(without alignments)  
1163.120 Million cell updates/sec

Title: US-09-884-050-2  
Perfect score: 792  
Sequence: 1 MNFLLSVHWSLALLYLHH.....FLOHKNCECRPKKDRARQEK 141

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n.model -DEV=xlh  
-O/Cyn2\_1/USPFO\_pool/US09884050/runat\_13112002\_133001\_14104/app\_query.fasta\_1.327  
-DB=N.Geneseq\_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09884050.ACGN.1.1.0.0/runat\_13112002\_133001\_14104 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THRAPDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq\_101002.\*

1: /SID22/cgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID22/cgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID22/cgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SID22/cgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SID22/cgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID22/cgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
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8: /SID22/cgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SID22/cgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
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19: /SID22/cgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SID22/cgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SID22/cgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID22/cgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID22/cgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID22/cgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	792	100.0	441	19	AAV38450	cDNA encoding huma
2	792	100.0	444	21	AAZ93345	Human vascular end
3	792	100.0	444	21	AAZ93345	Nucleotide sequenc
4	792	100.0	444	22	AAC90473	Human vascular end
5	792	100.0	444	22	AAC90477	Human VEGF121 DNA.
6	792	100.0	444	24	ABL57427	Human vascular end
7	792	100.0	473	16	AAQ99080	cDNA encoding huma
8	792	100.0	473	17	AAT17613	VEGF121 coding seq
9	792	100.0	473	21	AAI12853	cDNA encoding VEGF
10	792	100.0	495	20	AAZ29996	Nucleotide sequenc
11	792	100.0	516	19	AAZ28396	Vascular endotheli
12	792	100.0	516	20	AAZ57724	Human VEGF(145) co
13	792	100.0	544	22	AAH21876	Human VEGF splice
14	792	100.0	545	20	AAZ29999	Nucleotide sequenc
15	792	100.0	573	19	AAV38451	cDNA encoding huma
16	792	100.0	627	20	AAZ29997	Nucleotide sequenc
17	792	100.0	642	21	AAZ93348	Human vascular end
18	792	100.0	642	21	AAZ99547	Nucleotide sequenc
19	792	100.0	642	22	AAC90480	Human VEGF189 DNA.
20	792	100.0	642	24	ABL57430	Human vascular end
21	792	100.0	645	19	AAV38452	cDNA encoding huma
22	792	100.0	648	21	AAZ39835	Human A215 nucleot
23	792	100.0	648	22	AAC83521	Human VEGF C subun
24	792	100.0	666	20	AAZ29998	Nucleotide sequenc
25	792	100.0	677	16	AAQ99082	cDNA encoding huma
26	792	100.0	677	17	AAT17615	VEGF189 coding seq
27	792	100.0	677	21	AAI12855	cDNA encoding VEGF
28	792	100.0	696	21	AAV38453	cDNA encoding huma
29	792	100.0	699	21	AAZ93349	Human vascular end
30	792	100.0	699	21	AAZ99548	Nucleotide sequenc
31	792	100.0	699	22	AAC90481	Human VEGF206 DNA.
32	792	100.0	699	24	ABL57431	Human vascular end
33	792	100.0	728	16	AAQ99083	cDNA encoding huma
34	792	100.0	728	17	AAT17616	VEGF206 coding seq
35	792	100.0	728	21	AAI12856	cDNA encoding VEGF
36	792	100.0	774	18	AAT95644	Antisense inhibito
37	792	100.0	774	18	AAT97139	Human vascular end
38	792	100.0	774	19	AAV15102	Human vascular end
39	792	100.0	774	19	AAT95393	Human vascular end
40	792	100.0	815	22	AAI12883	DNA encoding for h
41	792	100.0	1195	11	AAQ84474	Human vascular per
42	792	100.0	1195	20	AAZ90498	Human vascular end
43	792	100.0	1873	19	AAV15103	Human vascular end
44	792	100.0	1873	20	AAZ21568	Vascular endotheli
45	789	99.6	774	17	AAT10120	Vascular endotheli

## ALIGNMENTS

## RESULT 1

AAV38450  
ID AAV38450 standard; cDNA; 441 BP.  
XX  
AC AAV38450;  
XX  
DT 11-SEP-1998 (first entry)  
XX  
DE cDNA encoding human VEGF-121.

XX Human; vascular endothelial growth factor; VEGF; production;  
XX nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;  
XX blood vessel; essential hypertension; pulmonary arterial hypertension;  
XX PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;  
XX coronary bypass operation; anastomosis; endarterectomy; ss.  
OS Homo sapiens.  
XX









XX The present sequence is the coding sequence of human vascular  
PS endothelial growth factor 121 (hVEGF121), an isoform that is weakly  
CC acidic and does not bind to heparin. The present invention  
CC concerns methods for the treatment of salt-sensitive hypertension  
CC by administering a VEGF in an amount effective to reduce the blood  
CC pressure of a salt-sensitive hypertension patient to a normal range.  
CC The VEGF is preferably hVEGF121 or a VEGF having a heparin-binding  
CC domain modified to render it incapable of binding heparin. The  
CC VEGF may be co-administered with another angiogenic factor. The  
CC method can also be used to treat disorders relating to abnormal  
CC transport of solutes across endothelial cells, including treatment  
CC or prevention of kidney disease associated with impaired filtration  
CC or excretion of solutes, central nervous system diseases associated  
CC with alterations in cerebrospinal fluid synthesis, composition or  
CC circulation including stroke, meningitis, tumour, infections, and  
CC disorders of bone growth, hypoxia or hypercapnia or fibrosis  
CC arising from accumulation of fluid secretions in lungs or  
CC syndrome, toxic alveolar injury as occurs in smoke inhalation,  
CC pneumonia, including viral and bacterial infections, surgical  
CC interventions, cystic fibrosis, and other inherited or acquired  
CC disease of the lung associated with fluid accumulation in the  
CC pulmonary air space, pulmonary endothelium injury, disordered  
CC transport of fluid and solutes across the intestinal epithelium,  
CC including inflammatory bowel disease, infections, diarrhoea,  
CC ascites accumulation in the peritoneum as occurs in the failure of  
CC heart, liver and kidney, preservation and enhancement of function  
CC of organ allografts, and cardiac valve disease.  
XX  
SQ Sequence 444 BP; 121 A; 113 C; 122 G; 88 T; 0 other;

Alignment Scores:  
Pred. No.: 1.76e-87 Length: 444  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-09-884-050-2 (1-141) x ABL57427 (1-444)

Qy 1 MetAsnPhLeuLeuSerTrpValHisTrpSerLeuLaLeuLeuLeuTyrLeuHisHis 20  
Dy 1 ATGAATTTCTGCTGCTTGGTGCATTGGAGCCTTGCTGCTGCTACCTCCACCAT 60  
Qy 21 AlalysTrpSerGlnAlaAlaPromMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Dy 61 GCCAAGTGTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGATCATCAGGAATG 120  
Qy 41 VallysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Dy 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCTCCATCCATCAGACCCCTGGTGAC 180  
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Dy 181 ATCTTCCAGGAGTACCTGTATGAGATGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Dy 241 ATGCGATCGGGGGTGTGTAATGACGAGGGGCTGGAGTGTGTGCCACCTGAGGAGTCC 300  
Qy 101 AsnIleThrMetGlnIleMetArgTleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Dy 301 AACATCACCATGCAATTTATCGGGATCAAACTCACCAGGCCACCATAGGAGATG 360  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Dy 361 AGCTTCCTACAGCACACAAATGTGAATGCAGACCAAGAAAGATAGACGAAGCAAGA 420  
Qy 141 Lys 141

Db 421 AAA 423  
RESULT 7  
AAQ99080  
ID AAQ99080 standard; cDNA; 473 BP.  
XX  
AC AAQ99080;  
XX  
DT 14-MAY-1996 (first entry)  
XX  
DE cDNA encoding human vascular endothelial growth factor-121, VEGF-121.  
KW Conjugate; growth factor; FGF; cytotoxin; saporin; eye; regulation;  
KW cell proliferation; psoriasis; pterygia; corneal clouding; cancer;  
KW rheumatoid arthritis; vascular endothelial; fibroblast; epidermal;  
KW heparin binding; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..456  
FT /\*tag= a  
FT /product= immature\_VEGF-121  
FT sig\_peptide 13..90  
FT /\*tag= b  
FT mat\_peptide 91..453  
FT /\*tag= c  
XX  
PN WO9524928-A2.  
XX  
XX 21-SEP-1995.  
XX  
XX 15-MAR-1995; 95WO-US03448.  
XX  
XX 15-MAR-1994; 94US-0213447.  
XX 15-MAR-1994; 94US-0213446.  
XX  
PA (PRIZ-) PRIZM PHARM INC.  
XX  
XX Baird JA, Houston LL, Nova MP, Sosnowski BA;  
XX  
XX WPI: 1995-336820/43.  
XX P-PSDB: AAR91075.  
XX  
XX New conjugates of growth factor receptor ligand and targetted agent  
XX - partic. DNA or cytotoxin, used to control cell proliferation in  
XX the eye, e.g. to prevent growth of pterygia and corneal clouding  
XX  
XX Disclosure: Page 184-185; 204pp; English.  
XX  
XX AAQ99080-099083 encode human vascular endothelial growth factors  
XX (VEGFs). DNA encoding a VEGF can be used to create a fusion protein  
XX (FP), the cDNA of which includes a nucleic acid binding domain (NABD)  
XX and encodes a heparin binding growth factor, HGF (e.g. VEGF, FGF,  
XX HBGF), a protein synthesis inhibitor and opt. a linker imparting  
XX flexibility to the FP. The FP can be used to target a protein synthesis  
XX inhibitor, an antisense DNA sequence or an inhibitor of elongation factor  
XX 2, to a cell carrying a HGF receptor. The conjugates of the invention  
XX are used to inhibit cell proliferation in cells carrying the particular  
XX growth factor receptor. A specific application is to prevent  
XX excessive proliferation of epithelial cells, fibroblasts and  
XX keratinocytes in the anterior eye after surgery, partic. to prevent  
XX recurrence of pterygia after surgical removal, closure of  
XX trabeculectomy after glaucoma surgery and corneal clouding after  
XX tumour laser treatment. Other conditions which may be treated include  
XX tumours, restenosis, psoriasis, Dupuytren's contracture, diabetic  
XX complications, Kaposi's sarcoma and rheumatoid arthritis.  
XX  
SQ Sequence 473 BP; 131 A; 119 C; 130 G; 93 T; 0 other;  
Alignment Scores:  
Pred. No.: 1.93e-87 Length: 473









CC disease in mammals, especially humans. They are also useful for enhancing  
 CC drug permeation by tumours. VEGF145 can also be administered to stimulate  
 CC vascular cell proliferation or to enhance endothelialization of diseased  
 CC vessels (especially re-endothelialization after angioplasty) in mammals.  
 CC VEGF145, which binds as weakly as VEGF165 to heparin, binds much better  
 CC than VEGF165 to the extracellular matrix (ECM). However, unlike VEGF189,  
 CC VEGF145 is secreted from producer cells and binds efficiently to ECM.  
 CC This combination of properties render VEGF145 the only known VEGF variant  
 CC that is secreted from producing cells retaining at the same time ECM  
 CC binding properties. This makes VEGF145 likely to diffuse towards the  
 CC target blood vessels, while some of the produced VEGF145 will be retained  
 CC by ECM components along the path of diffusion. This ECM bound pool will  
 CC dissociate slowly allowing a longer period of activity. Additionally, the  
 CC biological activity of VEGF145 is protected against oxidative damage  
 CC unlike VEGF forms such as VEGF121 thereby giving it a longer half-life.  
 XX

SQ Sequence 516 BP; 150 A; 125 C; 144 G; 97 T; 0 other;

Alignment Scores: 2.17e-87 Length: 516  
 Pred. No.: 792.00 Matches: 141  
 Score: 792.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 19

US-09-884-050-2 (1-141) x AAV28396 (1-516)

QY 1 MetAspPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 DB 1 ATGAACCTTCTGCTGCTTGGGTGCATTTGGAGCCTTGCCTTGCTGCTACCTCCACCAT 60  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
 DB 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCATCAGAGTG 120  
 QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 DB 121 GTCAAGTTCATGATGTCTATCAGCGCAGCTACTGCCATCCATCGAGACCCCTGGTGGAC 180  
 QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 DB 181 ATCTTCAGAGTACCTGTATGATGATCGATCATCTTCAAGCCATCTGCTGCCCCCTG 240  
 QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 DB 241 ATCGGATGCGGGGCTGCTCATGATGACGAGGCTGGAGTGTGCTGCCACTGAGGAGTCC 300  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 DB 301 AACATCACCATGCAGATTATGCGGATCAAAACCTCACCAAGGCCACATAGGAGAGATG 360  
 QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 DB 361 AGTTCTCTACAGCACACAAATGTGATGATGATGATGATGATGATGATGATGATGATG 420  
 QY 141 Lys 141  
 DB 421 AAA 423

RESULT 12

AAAX57724  
 ID AAAX57724 standard; cDNA; 516 BP.

XX

AC AAAX57724;

XX 03-AUG-1999 (first entry)

DT Human VEGF(145) coding sequence.

XX Human;vascular endothelial growth factor; VEGF; vector; stimulation;

XX angiogenesis; mammal; peripheral; cardiac; tissue; ischaemia; perfusion;

KW neovascularisation; muscle; ss.

KW

XX OS Homo sapiens.  
 XX FH Key.  
 FT CDS Location/Qualifiers  
 FT 1..516  
 FT /\*tag= a  
 FT /product= "human VEGF(145)"  
 FT 1..78  
 FT /\*tag= b  
 FT 78..516  
 FT /\*tag= c  
 FT mat\_peptide  
 FT sig\_peptide  
 XX WO9921590-A1.  
 XX 06-MAY-1999.  
 XX 23-OCT-1998; 98WO-US22668.  
 XX 26-NOV-1997; 97GB-0024906.  
 PR 27-OCT-1997; 97US-0063629.  
 XX (MERI ) MERCK & CO INC.  
 XX Bett AJ, Huckle WR, Kendall RL, Thomas KA;  
 PI WPI; 1999-302907/25.  
 DR P-PSDB; AAY07473.  
 XX Stimulating angiogenesis by expressing vascular endothelial growth  
 PT factor  
 PS Example 1; Fig 1; 46pp; English.  
 CC This sequence represents the coding sequence for the 145 amino acid form  
 CC of human vascular endothelial growth factor (VEGF(145)), which, when  
 CC administered in a vector, can be used to stimulate angiogenesis in a  
 CC mammal. Administration of the VEGF(145) is used to treat peripheral,  
 CC cardiac or other tissue ischaemias, i.e. to increase neovascularisation,  
 CC perfusion and performance of ischaemic muscle.  
 XX SQ Sequence 516 BP; 150 A; 126 C; 143 G; 97 T; 0 other;

Alignment Scores: 2.17e-87 Length: 516  
 Pred. No.: 792.00 Matches: 141  
 Score: 792.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 20

US-09-884-050-2 (1-141) x AAX57724 (1-516)

QY 1 MetAspPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 DB 1 ATGAACCTTCTGCTGCTTGGGTGCATTTGGAGCCTTGCCTTGCTGCTACCTCCACCAT 60  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
 DB 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCATCAGAGTG 120  
 QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 DB 121 GTCAAGTTCATGATGTCTATCAGCGCAGCTACTGCCATCCATCGAGACCCCTGGTGGAC 180  
 QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 DB 181 ATCTTCAGAGTACCTGTATGATGATCGATCATCTTCAAGCCATCTGCTGCCCCCTG 240  
 QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 DB 241 ATCGGATGCGGGGCTGCTCATGATGACGAGGCTGGAGTGTGCTGCCACTGAGGAGTCC 300  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120

```

|||||
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 360
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 361 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGCAAGACAAGAA 420
QY 141 Lys 141
|||
Db 421 AAA 423

RESULT 13
AAH21876
ID AAH21876 standard; cDNA; 544 BP.
XX
AC AAH21876;
XX
DT 16-AUG-2001 (first entry)
DE Human VEGF splice variant VEGF121 encoding cDNA SEQ ID NO:3.
XX
KW Human; vascular endothelial growth factor; VEGF splice variant; VEGF;
KW VEGF121; colon cancer cell line acquired malignancy; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..452
FT /tag= a
FT sig_peptide /product= "VEGF splice variant VEGF121"
FT 9..86
FT /tag= b
FT mat_peptide 87..449
FT /tag= c
XX
XX JP2001061483-A.
XX
XX 13-MAR-2001.
XX
XX 31-AUG-1999; 99JP-0244198.
XX
XX 31-AUG-1999; 99JP-0244198.
XX
XX (EISA ) EISAI CO LTD.
XX
XX WPI: 2001-294711/31.
XX P-PSDB: AAB98080.
XX
XX Human colon cancer cell line is transfected with VEGF gene and selected
XX for having acquired malignancy -
XX
XX Example 1; Page 6; 8pp; Japanese.
XX
CC The present invention describes a method in which the vascular
CC endothelial growth cell (VEGF) gene is introduced to a human colon
CC cancer cell showing no malignancy, and a cell line highly expressing
CC VEGF is selected to get a cell line acquired malignancy. Also described
CC are: (1) a human colon cancer cell line acquired malignancy by the above
CC method; (2) WiDr cell line acquired malignancy by the above method;
CC (3) a method for screening an anticancer agent by using the above human
CC colon cancer cell line, preferably WiDr cell line, acquired malignancy;
CC and (4) a compound screened by the above method. The human colon cancer
CC cell line acquired malignancy can be used for screening an anticancer
CC agent. The present sequence encodes the human VEGF splice variant
CC VEGF121, which is used in an example from the present invention.
XX
SQ Sequence 544 BP; 150 A; 141 C; 150 G; 103 T; 0 other;

Alignment Scores:
Pred. No.: 2,33e-87 Length: 544
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-884-050-2 (1-141) x AAH21876 (1-544)
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Db 9 ATGAACCTTCTGCTGTCTGGTGCATTGGAGCCCTTGCTTGCCTCTACCTCAGCAT 68
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40
Db 69 GCCAAGTGGTCCCGAGCTGCACCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 128
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
Db 129 GTGAAGTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCATCGAGACCCTGGTGAC 188
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 189 ATCTTCCAGGAGTACCTGTATGATGAGATGAGTACATCTTCAAGCCATCCTGTGCCCCG 248
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
Db 249 ATGCGATGCGGGGGCTGCTGCATGACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 308
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 309 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 368
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 369 AGCTTCTTACAGCACAAATGTGAATGCAGACCAAGAAAGATAGCAAGACAAGAA 428
QY 141 Lys 141
|||
Db 429 AAA 431

RESULT 14
AAZ29999
ID AAZ29999 standard; DNA; 545 BP.
XX
AC AAZ29999;
XX
XX 26-JAN-2000 (first entry)
XX
XX Nucleotide sequence of VEGF-A145.
XX
KW Vascular endothelial factor; VEGF; VEGF-A145; variant; vascular disease;
KW cardiovascular disease; vascular cell proliferation; angioplasty;
KW restenosis; drug permeation; tumour; ischemic condition;
KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;
KW chronic lower limb ischemia; peripheral vascular disease; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9940197-A2.
XX
XX PD 12-AUG-1999.
XX
XX PF 04-FEB-1999; 99WO-US02425.
XX
XX PR 06-FEB-1998; 98US-0073979.
XX
XX (COLL-) COLLATERAL THERAPEUTICS INC.
XX
XX PI Baird A, Andreason G;
XX
XX WPI: 1999-600967/51.
XX
XX New growth factor variants, useful for treating cardiovascular disease,
XX especially by stimulating vascular cell proliferation -
XX
XX Example 1; Page 70; 101pp; English.

```



QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
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Db 241 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCACTGAGGAGTCC 300  
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QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
|||||  
Db 301 AACATCACCATTGCAGATTATGCGGATCAAACTCACCAGGCCACACATAGGAGAGATG 360  
|||||  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
|||||  
Db 361 AGCTTCCTACAGCACACAAATGTGATGCAGACCAAGAAAGATAGAGCAAGACAGAA 420  
|||||  
QY 141 Lys 141  
|||  
Db 421 AAA 423

Search completed: November 20, 2002, 05:07:28  
Job time : 281 secs

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 05:00:39 ; Search time 2673 seconds  
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1535.165 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLLSNVHWSLALLYLHH.....FLOHNKCECRPKKDRARQEK 141

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-WARN\_TIMEOUT=30 -THREMS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
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Database :

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2: gb\_htg.\*

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6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

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12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	792	100.0	441	6	A92242	1	A92242 Sequence 1
2	792	100.0	444	6	AR198591	1	AR198591 Sequence
3	792	100.0	444	6	AX048686	1	AX048686 Sequence
4	792	100.0	444	6	AX050391	1	AX050391 Sequence
5	792	100.0	444	9	AF214570	1	AF214570 Homo sapi
6	792	100.0	516	6	AX029451	1	AX029451 Sequence
7	792	100.0	544	6	E49139	1	E49139 Human large
8	792	100.0	573	6	A92244	1	A92244 Sequence 3
9	792	100.0	630	9	HS010438	1	HS010438 Homo sapi
10	792	100.0	642	6	AR198594	1	AR198594 Sequence
11	792	100.0	642	6	AX050397	1	AX050397 Sequence
12	792	100.0	645	6	A92246	1	A92246 Sequence 5
13	792	100.0	648	6	AR117116	1	AR117116 Sequence
14	792	100.0	696	6	A92248	1	A92248 Sequence 7
15	792	100.0	699	6	AR198595	1	AR198595 Sequence
16	792	100.0	699	6	AX050399	1	AX050399 Sequence
17	792	100.0	774	6	AR118875	1	AR118875 Sequence
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19	792	100.0	774	6	E13215	1	E13215 Human mRNA
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21	792	100.0	774	6	E14233	1	E14233 Human mRNA
22	792	100.0	774	6	E15156	1	E15156 Human VEGF
23	792	100.0	815	6	AX234496	1	AX234496 Sequence
24	792	100.0	815	9	S85192	1	S85192 Homo sapien
25	792	100.0	1195	9	HUMVEF	1	HUMVEF Human vascu
26	792	100.0	1873	6	E15157	1	E15157 Human VEGF
27	792	100.0	1873	6	E22645	1	E22645 Antisense n
28	787	99.4	541	6	AX204783	1	AX204783 Sequence
29	787	99.4	541	9	AF091352	1	AF091352 Homo sapi
30	787	99.4	573	6	AX060342	1	AX060342 Sequence
31	787	99.4	576	6	AR198593	1	AR198593 Sequence
32	787	99.4	576	6	AX050395	1	AX050395 Sequence
33	787	99.4	576	6	AX481507	1	AX481507 Sequence
34	787	99.4	576	9	AB021221	1	AB021221 Homo sapi
35	787	99.4	576	9	AF486837	1	AF486837 Homo sapi
36	787	99.4	576	9	S82167	1	S82167 simVEGF165-
37	787	99.4	606	9	AF430806	1	AF430806 Homo sapi
38	787	99.4	640	9	AY047581	1	AY047581 Homo sapi
39	787	99.4	649	9	HSVEGF	1	HSVEGF H.sapiens v
40	787	99.4	990	6	AX039419	1	AX039419 Sequence
41	787	99.4	990	6	AX135799	1	AX135799 Sequence
42	787	99.4	990	6	AX234351	1	AX234351 Sequence
43	787	99.4	990	6	AX409689	1	AX409689 Sequence
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ALIGNMENTS

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A92242 LOCUS A92242 441 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1 from Patent WO9820027.  
ACCESSION A92242  
VERSION A92242.1 GI:6741017  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 441)  
AUTHORS Ylae-Herttua, S. and Martin, J.F.  
TITLE THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY FOR THE TREATMENT OF INTIMAL HYPERPLASIA  
JOURNAL Patent: WO 9820027-A 1 14-MAY-1998:  
FEATURES  
source YLAE HERTTUALA SEPPA (FI); MARTIN JOHN FRANCIS (GB)  
1. .441 Location/Qualifiers  
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Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservatives: 0  
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Db 361 AGCTTCCTACAGCACACAACAAATGTGAATGCAGACCAACAAAGAAAGATAGACGAACAGAA 420  
QY 141 Lys 141  
Db 421 AAA 423  
RESULT 2

AR198591 LOCUS AR198591 444 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6 from patent US 6352975.  
ACCESSION AR198591  
VERSION AR198591.1 GI:20248440  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 444)  
AUTHORS Schreiner, G.F. and Johnson, R.J.  
TITLE Methods of treating hypertension and compositions for use therein  
JOURNAL Patent: US 6352975-A 6 05-MAR-2002:  
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DB: 6 Gaps: 0  
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Db 61 GCCAAGTGTCTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCAGAGTG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTCAAGTTCATGATGCTATATCAGCGCAGCTACTGCCATCCATCGAGACCTGGTGGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTTCAGAGGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCCGATGGGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGCTCCACTGAGGAGTCC 300  
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QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCCTACAGCACACAACAAATGTGAATGCAGACCAACAAAGAAAGATAGACGAACAGAA 420  
QY 141 Lys 141  
Db 421 AAA 423  
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LOCUS AX048686 444 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 3 from Patent WO0071716.  
ACCESSION AX048686  
VERSION AX048686.1 GI:12225840  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 444)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.









LOCUS HSA010438 630 bp mRNA linear PRI 15-JAN-1999  
DEFINITION Homo sapiens mRNA for vascular endothelial growth factor, splicing  
variant VEGF183.  
ACCESSION AJ010438  
VERSION AJ010438.1 GI:3647280  
KEYWORDS vascular endothelial growth factor; vegf gene; VEGF183 protein.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
AUTHORS Lei, J., Jiang, A. and Pei, D.  
TITLE Direct Submission\*  
JOURNAL Submitted (20-AUG-1998) Pei D., Pharmacology, University of  
Minnesota, 3-249 Millard Hall, 435 Delaware St. S.E., Minneapolis,  
MN55455, USA  
REFERENCE 2 (bases 1 to 630)  
AUTHORS Lei, J., Jiang, A. and Pei, D.  
TITLE Identification and characterization of a new splicing variant of  
vascular endothelial growth factor: VEGF183  
JOURNAL Biochim. Biophys. Acta 1443 (3), 400-406 (1998)  
MEDLINE 99096474  
PUBMED 9878851  
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DB:  
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QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGGTCCAGGCTGCCATGGCAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTGAAGTTTCATGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTCCAGAGTACCTGATGAGATCGAGTACATCTTCAAGGCATCTCTGTGCGCCCTG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCGCATCGGGGGCTGCTGCAATGACGAGGGCTGTGGAGTGTGTGCCCATCTAGGAGTCC 300  
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Db 421 AAA 423  
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ACCESSION AR198594  
VERSION AR198594.1 GI:20248443  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 642)  
AUTHORS Schreiner, G.F. and Johnson, R.J.  
TITLE Methods of treating hypertension and compositions for use therein  
JOURNAL Patent: US 6352975-A 9 05-MAR-2002;  
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 REFERENCE  
 1 (bases 1 to 642)  
 AUTHORS Pollitt,N.S. and Abraham,J.A.  
 TITLE Vascular endothelial growth factor variants  
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 SCIOS INC. (US)  
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 VERSION A92246.1 GI:6741021  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE  
 1 (bases 1 to 645)  
 AUTHORS Ylae-Herttuala,S. and Martin,J.F.  
 TITLE THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY  
 FOR THE TREATMENT OF INTIMAL HYPERPLASIA  
 JOURNAL Patent: WO 9820027-A 5 14-MAY-1998;  
 YLAE HERTTUALA SEPPO (FI); MARTIN JOHN FRANCIS (GB)  
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 BASE COUNT 185 a 155 c 181 g 124 t  
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 Score: 792.00 Matches: 141  
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 Db 61 GCCAAGTGTCCAGGCTGCACCCATGCGCAGAGGAGGAGGCGCAGAAATCATCAGCAAGTG 120  
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 Db 241 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 300  
 Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
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GenCore version 5.1.3  
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Run on: November 20, 2002, 04:59:33 ; Search time 56 seconds  
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Title: us-09-884-050-2

Perfect score: 792

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Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	792	100.0	815	10	US-09-795-006A-146 Sequence 146, App
3	787	99.4	480	10	US-09-365-029-93 Sequence 93, Appli
4	787	99.4	576	10	US-09-932-451A-1 Sequence 1, Appli

5	787	99.4	649	10	US-09-349-954A-1 Sequence 1, Appli
6	787	99.4	649	10	US-09-907-007-1 Sequence 1, Appli
7	787	99.4	990	10	US-09-880-107-2336 Sequence 2336, Ap
8	787	99.4	990	10	US-09-795-006A-1 Sequence 1, Appli
9	787	99.4	1736	12	US-10-044-090-164 Sequence 164, App
10	787	99.4	3583	9	US-09-981-353-185 Sequence 185, App
11	715	90.3	459	10	US-09-867-701-10298 Sequence 10298, A
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13	583	73.6	388	10	US-09-795-006A-82 Sequence 82, Appl
14	521.5	65.8	391	10	US-09-795-006A-82 Sequence 82, Appl
15	512.5	64.7	391	10	US-09-795-006A-86 Sequence 86, Appl
16	506	63.9	322	10	US-09-795-006A-50 Sequence 50, Appl
17	501	63.3	388	10	US-09-795-006A-54 Sequence 54, Appl
18	474.5	59.9	391	10	US-09-795-006A-90 Sequence 90, Appl
19	465.5	58.8	391	10	US-09-795-006A-94 Sequence 94, Appl
20	460.5	58.1	391	10	US-09-795-006A-84 Sequence 84, Appl
21	459	58.0	322	10	US-09-795-006A-58 Sequence 58, Appl
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23	452	57.1	328	10	US-09-795-006A-152 Sequence 152, App
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#### ALIGNMENTS

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; Patent No. US20020065240A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Kenneth A., Jr.
; APPLICANT: Kendall, Richard L.
; APPLICANT: Bett, Andrew J.
; APPLICANT: Huckle, William R.
; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF ANGIOGENESIS
; FILE REFERENCE: 20073P
; CURRENT APPLICATION NUMBER: US/09/812,133
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/22668
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/063,629
; PRIOR FILING DATE: 1997-10-27
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: GENERAL INFORMATION:			
: APPLICANT: Hayward, Nicholas K.			
: APPLICANT: Weber, Gunther			
: APPLICANT: Grimmond, Sean			
: APPLICANT: No. US20020019027A1denskjold, Magnus			
: APPLICANT: Larsson, Catharina			
: TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING			
: SAME			
: FILE REFERENCE: Dav. Col. Cave			
: CURRENT APPLICATION NUMBER: US/09/349,954A			
: CURRENT FILING DATE: 1999-07-08			
: PRIOR APPLICATION NUMBER: 08/765,588			
: PRIOR FILING DATE: 1996-02-22			
: NUMBER OF SEQ ID NOS: 22			
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: ORGANISM: Nucleotide Sequence of VEGF165			
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; Patent No. US20020142395A1
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; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020142395Aldenskjoeld, Magnus
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: SAME
; CURRENT APPLICATION NUMBER: US/09/907,007
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; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
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Db 137 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTGTGGTGG 196
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 197 ATCTTCCAGGAGTACCTGTATGAGATCGAGTACATCTTCAAGCCCATCTGTGTGCCCTG 256
QY 81 MetArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluMet 100
Db 257 ATGCGATGCGGGGGTGTGTCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 316
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 317 AACATCACCATGCGATGATGCGATCAACCTCACCAGGCCAGCAGCATAGGAGATG 376
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```
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 377 AGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGAGACAAGAA 436
RESULT 7
US-09-880-107-2336
; Sequence 2336, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2336
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M32977
US-09-880-107-2336
Alignment Scores:
Pred. No.: 3,88e-96 Length: 990
Score: 787.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.37% Indels: 0
DB: 10 Gaps: 0
US-09-884-050-2 (1-141) x US-09-880-107-2336 (1-990)
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTyrLeuHisHis 20
Db 57 ATGAACCTTTCTGCTGTCTTGGTGCATTGGAGCCTGCGCTTGTCTACCTCCACCAT 116
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
Db 117 GCCAAGTGTCTCCAGGCTGCACCTATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 176
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
Db 177 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTGTGGTGG 236
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 237 ATCTTCCAGGAGTACCTGTATGAGATCGAGTACATCTTCAAGCCCATCTGTGTGCCCTG 296
QY 81 MetArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
Db 297 ATGCGATGCGGGGGTGTGTCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 356
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 357 AACATCACCATGCGATGATGCGATCAACCTCACCAGGCCAGCAGCATAGGAGATG 416
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 417 AGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGAGACAAGAA 476
RESULT 8
US-09-795-006A-1
; Sequence 1, Application US/09795006A
; Patent No. US20020151680A1
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;	LENGTH: 1736	
;	TYPE: DNA	
;	ORGANISM: Homo sapiens	
;	FEATURE:	
;	NAME/KEY: misc.feature	
;	OTHER INFORMATION: Incyte ID No. US20020137081A1 3348156CBI	
;	NAME/KEY: unsure	
;	LOCATION: 1434, 1438-1439, 1512, 1514, 1521-1522, 1530	
;	OTHER INFORMATION: a, t, c, g, or other	
US-10-044-090-164		
Alignment Scores:		
Pred. No.:	8,95e-96	Length: 1736
Score:	787.00	Matches: 140
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	99.37%	Indels: 0
DB:	12	Gaps: 0
US-09-884-050-2 (1-141) x US-10-044-090-164 (1-1736)		
Qy	1 MetAsnPheLeuLeuSerTIpValHisTIpSerLeuAlaLeuLeuLeuTyrlLeuHisHis	20
Db	150 ATGAACTTCTGCTGCTCTGGGTGCATTTGGAGCCTTGCCCTTGCTGTACCTCCACCAT	209
Qy	21 AlalysTIpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal	40
Db	210 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGCAGAAATCATCACGAAGTG	269
Qy	41 VallysPheMetAspValTyrlGlnArgSerTyrlCysHisProIleGluThrLeuValAsp	60
Db	270 GTGAAGTTCATGGATGTCTATCAGCGCAGCTACTGTCATCCAATCAGACCCCTGGTGGAC	329
Qy	61 IlePheGlnGluTyrlProAspGluIleGluTyrlIlePheLysProSerCysValProLeu	80
Db	330 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG	389
Qy	81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer	100
Db	390 ATGCGATGCGGGGCTGCTCAATGACGAGGGCTGGAGTGTGTGCCACTGAGGAGTCC	449
Qy	101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet	120
Db	450 AACATCACCATGCGAGATTATGCGGATCAAACTTCACCAAGGCCAGCACATAGGAGAGATG	509
Qy	121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu	140
Db	510 AGCTTCTACAGCACACAAATGTGAATGCAGACCACCAAGAAAGATAGACCAAGACAAGAA	569
RESULT 10		
US-09-981-353-185		
;	Sequence 185, Application US/09981353	
;	Patent No. US20020160382A1	
;	GENERAL INFORMATION:	
;	APPLICANT: Lasek, Amy W.	
;	APPLICANT: Jones, David A.	
;	TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER	
;	FILE REFERENCE: PA-0038 US	
;	CURRENT APPLICATION NUMBER: US/09/981,353	
;	CURRENT FILING DATE: 2001-10-11	
;	NUMBER OF SEQ ID NOS: 194	
;	SOFTWARE: PERL Program	
;	SEQ ID NO 185	
;	LENGTH: 3583	
;	TYPE: DNA	
;	ORGANISM: Homo sapiens	
;	FEATURE:	
;	NAME/KEY: misc.feature	
;	OTHER INFORMATION: Incyte ID No. US20020160382A1 1384719.3	
;	NAME/KEY: unsure	
;	LOCATION: 3245, 3265	
;	OTHER INFORMATION: a, t, c, g, or other	
US-09-981-353-185		

US-09-884-050-2 (1-141) x US-09-867-701-10298 (1-459)

Qy	94	CysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleIleYsProHisGln	113
Db	188	TGCCTTCCCCACCCAGGAGTCCACATCACCATGCAGATTATGAGATTAAACCTCACCA	247
Qy	114	GlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgProLys	133
Db	248	GGCGAGCACATCGAGAGATGAGCTTCTCCAGCATAAACAAATGTCAATGTAGACCAAAG	307
Qy	134	LysAspArgAlaArgGlnGluLys	141
Db	308	AAAGATTGTGCTTCGAACAAAAA	331
RESULT 14			
US-09-795-006A-82			
; Sequence 82, Application US/09795006A			
; Patent No. US20020151680A1			
; GENERAL INFORMATION:			
; APPLICANT: Altaiato et al			
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR			
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS			
; FILE REFERENCE: 28967/359778			
; CURRENT APPLICATION NUMBER: US/09/795,006A			
; CURRENT FILING DATE: 2001-02-26			

```

? PRIOR APPLICATION NUMBER: US 00/203,331
? PRIOR FILING DATE: 2000-05-18
? PRIOR APPLICATION NUMBER: US 60/185,205
? PRIOR FILING DATE: 2000-02-25
? NUMBER OF SEQ ID NOS: 175
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 82
? LENGTH: 391
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
? NAME/KEY: CDS
? LOCATION: (8)..(388)
US-09-795-006A-82

Alignment Scores:
Pred. No.: 3,79e-61
Score: 521.50
Percent Similarity: 92.66%
Best Local Similarity: 86.24%
Query Match: 65.85%
DB: 10
Gaps: 1
Indels: 1
Mismatches: 7
Conservative: 7
Matches: 94
Length: 391

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Db	8	GGGCAGAAATCATACGAAAGTGGTGAATCTATTGTAATAGTGAGGAAGAGCTCAGTCG	67
Qy	53	HisProIleGluThrLeuValAspIlePheGlnGluTyPrAspGluIleGluTyIle	72
Db	68	ATGCCGATCGAGACACTGGTGGACATCTCCAGGAATACCCCTCATGAGATCGAGTACATC	127
Qy	73	PhelysProSerCysValProLeuMetArgCysGlyClyCysCysAsnAspGluGlyLeu	92
Db	128	TTCAAGCCATCTCGTGGCCCTGTATGAGATGTGGGGGTTCCTGCAATGACGAAGGGCTG	187
Qy	93	GluCysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHis	112
Db	188	GAGTGCCTTCCACCCGAGGAGTCCAACATCACCATCGAGATTTATGAGAATTTAAACCTCAC	247
Qy	113	GlnGlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgPro	132
Db	248	CAAGGCAGCACATCGAGAGATGAGCTTTCTCAGCATACAAATGTGAATGAGACCA	307
Qy	133	LysLysAspArgAlaArgGlnGluLys	141
Db	308	AAGAAAGATTTGGTCTTCGACAAAAA	334

## RESULT 15

US-09-795-006A-86  
; Sequence 86, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 391  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA  
; NAME/KEY: CDS  
; LOCATION: (8)..(388)  
US-09-795-006A-86

Alignment Scores:  
Pred. No.: 6 09e-60 Length: 391  
Score: 512.50 Matches: 92  
Percent Similarity: 91.74% Conservative: 8  
Best Local Similarity: 84.40% Mismatches: 8  
Query Match: 64.71% Indels: 1  
DB: 10 Gaps: 1

US-09-884-050-2 (1-141) x US-09-795-006A-86 (1-391)

QY	34	GlyGlnAsnHisGluValValLysPheMetAsp---ValTyrGlnArgSerTyrCys	52
DB	8	GGGCAGAAATCATCACCAAGTGGTGAATCTATTGATAATGAGTGGAGAAAGACTCAGTGC	67
QY	53	HisProIleGluThrLeuValAspIlePheGlnGluTyrProAspGluIleGluTyrIle	72
DB	68	ATGCCGATCGAGACACTGTGGACATCTCCAGGAATACCCCTGATGAGATCGAGTACATC	127
QY	73	PheLysProSerCysValProLeuMetArgCysGlyGlyCysCysAsnAspGluGlyLeu	92
DB	128	TTCAAGCCATCTCTGCTGCCCTCGATGAGATGTGGGGTTCGTCATAGTAGGGGCTG	187
QY	93	GluCysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHis	112
DB	188	CAGTGGCTTCCCAACCCAGGAGTCCAAACATCACCATGCAGATTATGAGATTAAACCTCAC	247
QY	113	GlnGlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgPro	132
DB	248	CAAGGGCAGACATCGAGAGATGAGCTTCTCCAGCATAACAAATGTGAATGTAGACCA	307
QY	133	LysLysAspArgAlaArgGlnGluLys	141
DB	308	AAGAAGATTGTGCTTCGACAAAAA	334

Search completed: November 20, 2002, 05:08:46  
Job time : 62 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 05:01:43 ; Search time 2138 Seconds  
(without alignments)  
1068.084 Million cell updates/sec

Title: US-09-884-050-2  
Perfect score: 792  
Sequence: 1 MNFLSWVHWSLALLYLHH.....FLQHNKCECRPKKDRARQEK 141

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_othr:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	94.6	749	528	14	BQ674897 AGENCOURT
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3	86.0	681.5	752	14	BQ780197
4	73.8	584.5	600	12	BG803325 0223-76 M
5	69.7	552	890	13	BI869727 603393614
6	63.6	503.5	719	12	BG864739 602799154
7	49.3	390.5	600	12	BG802357 0174-04 M
8	48.6	385	534	14	BM991154 UI-H-D10-
9	48.2	382	649	12	BF679862 602154448
10	44.6	353	208	10	BE166230 MR3-HT048
11	41.0	325	869	9	AL552344 AL552344
12	41.0	325	890	14	BQ644755 AGENCOURT
13	41.0	325	901	9	AL552106
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15	41.0	325	925	9	AL547463
16	41.0	325	963	9	AL540600
17	41.0	325	963	14	BQ893335
18	41.0	325	1023	9	AL543185
19	41.0	325	1031	14	BQ070531
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21	40.2	318.5	489	13	BI790853
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24	39.9	316	900	14	BQ647895
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26	39.6	314	887	14	BQ881520
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30	39.4	312	455	9	AI272466
31	39.4	312	885	9	AL543693
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36	37.9	300	953	14	BQ713895
37	37.8	299	794	13	BI852987
38	37.8	299	913	9	AL553367
39	37.1	294	724	13	BI692908
40	37.0	293	364	9	AL838330
41	36.9	291	950	9	AL551942
42	36.7	291	733	13	BG923923
43	36.7	290.5	874	10	BE570632
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ALIGNMENTS

RESULT 1  
BQ674897

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

BQ674897 528 bp mRNA linear EST 15-JUL-2002  
AGENCOURT\_8036450 NIH\_MGC\_102 Homo sapiens CDNA clone IMAGE:6212223  
5' mRNA sequence.

BQ674897

BQ674897.1 GI:21785731

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)



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Db 182 ATGCGATCGGGGCTGCTGCAATACGAGGCCCTGGAGTGTGTGCCACTGAGGAGT 123
Qy 100 eRAsnileThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluM 120
Db 122 CCAACATCCCATGAGATTATGCGATCAACCTCACCAGGCCGACACATAGAGAGA 63
Qy 120 etSerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnG 140
Db 62 TGAGCTTCTACAGCCCAACAATGTGAATGCAGACCAAAAAAAAAAAAAAAAAAAAAA 3
Qy 140 lu 140
Db 2 AA 1

RESULT 3
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DEFINITION UI-R-PF0-cpb-i-06-0-UI.s1 UI-R-PF0 Rattus norvegicus cDNA clone
ACCESSION BQ780197
VERSION BQ780197.1 GI:21988669
KEYWORDS EST
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 752)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Jeff Stevens
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: DISTRIBUTION: Researchers may obtain clones
from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-39, >POLY_A#Simple_repeat (matched complement) 546-578,
>GC_rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA-Yes.
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Location/Qualifiers
1..752
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="UI-R-PF0-cpb-i-06-0-UI"
/clone_lib="UI-R-PF0"
/tissue_type="Mixed tissues"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site.1: EcoR I; Site.2: Not I; UI-R-PF0 is a
subtracted cDNA library containing the following tissue(s)
): Normal cartilage and SR-JWS Tumor Line . The
subtraction was made according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for these libraries are: CTAATGGAGC,
CAATCTTGTA.
TAG_LIB=UI-R-PF0

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TAG_TISSUE=cartilage
TAG_SEQ=CTAATGGAGC"
BASE COUNT 109 a 246 c 205 g 189 t 3 others
ORIGIN
Alignment Scores:
Pred. No.: 4.6e-74 Length: 752
Score: 681.50 Matches: 122
Percent Similarity: 90.78% Conservative: 6
Best Local Similarity: 86.52% Mismatches: 12
Query Match: 86.05% Indels: 1
Db: 14 Gaps: 1
US-09-884-050-2 (1-141) x BQ780197 (1-752)
Qy 1 MetAsnPheLeuSerTyrValHisTyrPheLeuAlaLeuLeuTyrLeuHisHis 20
Db 431 ATGAACCTTCTGCTCTCTTGGTGCACCTGGGCCCTTGTACTGCTGTACCTCCACCAT 372
Qy 21 AlaLysTyrSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
Db 371 GCCAAGTGTCCCGCTGCACCCACGACAGAA---GGGGACGACAGAAAGG 315
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValasp 60
Db 314 GTGAAGTTTCATGGAGCTCTACCAGCGCAGCTATTGCCGTCCAATTGAGACCTGGTGGAC 255
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 254 ATCTTCCAGGAGTACCCCGATGAGATAGATATATCTTCAAGCCGCTCTGTGCCCTTA 195
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
Db 194 ATGCGGTGTGGGGTGTGCAATGATGAGCCCTGGAGTGGTCCCGACGTCGGAGAC 135
Qy 101 AsnIleThrMetGlnIleMetArgLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 134 AACGTCTCATGTCAGATCATGGGATCAAACTCAACCAAGCCAGCACATAGGAGAGTG 75
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 74 AGCTTCTGCGACGATAGCAGATGTGAATGCAGACCAAGAAAGATAGAACAAAGCCAAA 15
Qy 141 Lys 141
Db 14 AAA 12
RESULT 4
BQ803325
LOCUS BQ803325 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 0223-76 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
ACCESSION BQ803325
VERSION BQ803325.1 GI:17950226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
FEATURES

```

```

source
1..600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/notes="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dt. RNA isolation: cytoplasmic RNA preps
(Mannatis); Cloning Technique: CUA Cloning (Clontech,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TAGCTCCAGTGAATCTGAGTG--->. Other
information regarding entire library may be found at
http://pga.smed.edu/data/libraries/microarray_cdna_library.htm."
BASE COUNT 131 a 183 c 196 g 90 t
ORIGIN

Alignment Scores:
Pred. No.: 3,71e-62 Length: 600
Score: 584.50 Matches: 106
Percent Similarity: 90.76% Conservativity: 2
Best Local Similarity: 89.08% Mismatches: 10
Query Match: 73.80% Indels: 1
DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG803325 (1-600)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20
|||||
Db 246 ATGAACCTTCTGCTCTCTGGTGCACCTGGACCTGCTTACTGCTGACCTCCACCAT 305
|||||

Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
|||||
Db 306 GCCAAGTGGTCCCGAGGTGCACCCACACAGAA---GGAGAGCAGAGTCCCATGAAGTG 362
|||||

Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
|||||
Db 363 ATCAAGTTCATGGATGCTACCGAGGAGTACTGCGCTCCGATGAGACCTGGTGGAC 422
|||||

Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
|||||
Db 423 ATCTTCAGAGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCTGTGCGCGCTG 482
|||||

Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
|||||
Db 483 ATGCGCTGTCGAGGCTGCTACAGATGAGAGCCCTGGAGTGGTCCGCTCAGAGAGC 542
|||||

Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGlu 119
|||||
Db 543 AACATCACCATGCAGATCATGCGGATCAAAACCTCACCAGAGCCAGCACATAGAGAG 599
|||||

RESULT 5
BI869727 890 bp mRNA linear EST 11-OCT-2001
LOCUS 603393614F1 NTH_MGC_90 Homo sapiens cdna clone IMAGE:5403771 5',
DEFINITION mRNA sequence.
ACCESSION BI869727
VERSION BI869727.1 GI:16043400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12029 row: k column: 04

High quality sequence stop: 733.

#### FEATURES

Location/Qualifiers  
 source 1..890  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:5403771"  
 /clone\_lib="NIH\_MGC\_90"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /notes="Organ: liver; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
 BASE COUNT 246 a 246 c 256 g 142 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7.46e-58 Length: 890  
 Score: 552.00 Matches: 98  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 69.70% Indels: 0  
 DB: 13 Gaps: 0

US-09-884-050-2 (1-141) x BI869727 (1-890)

Qy 43 PheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIlePhe 62  
 |||||

Db 1 TTCATGGATGTCTATCAGCGCAGCTACTCCATCCATCCAGACCTGGTGGACATCTTC 60  
 |||||

Qy 63 GlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMetArg 82  
 |||||

Db 61 CAGGAGTACCCCTGATGAGATCAGTACATCTTCAAGCCATCCTGTGTCCTGATGCCA 120  
 |||||

Qy 83 CysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsnIle 102  
 |||||

Db 121 TCGGGGGCTGCTGCATGACGAGGCGCTGGAGTGTGCCACCTGAGAGTCCCAATC 180  
 |||||

Qy 103 ThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSerPhe 122  
 |||||

Db 181 ACCATGCAGATTATCGGATCAAACTCACCAGGCCAGCACATAGAGAGATGAGCTTC 240  
 |||||

Qy 123 LeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 |||||

Db 241 CTACAGCACAAATGTGATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 294  
 |||||

#### RESULT 6

BI864739

LOCUS BG864739

DEFINITION 602799154F1 NCI\_CGAP\_Mam4 Mus musculus cdna clone IMAGE:4934916 5',

DEFINITION mRNA sequence.

ACCESSION BI864739

VERSION BG864739.1 GI:14215277

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 719)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth

Ph.D.

cdna Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10864 Row: k Column: 13  
 High quality sequence stop: 715.  
 Location/Qualifiers  
 1. 719

#### FEATURES

source  
 1. 719  
 /organism="Mus musculus"  
 /strain="NMRI"  
 /db\_xref="taxon:10090"  
 /clone\_lib="NCI\_CGAP\_Mam4"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Sali;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."

BASE COUNT 156 a 205 c 245 g 113 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 5.74e-52 Length: 719  
 Score: 503.50 Matches: 91  
 Percent Similarity: 90.29% Conservative: 2  
 Best Local Similarity: 88.35% Mismatches: 9  
 Query Match: 63.57% Indels: 1  
 DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG864739 (1-719)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyLeuHisHis 20  
 Db 312 ATGAACCTTCTGCTCTCTGGTGCACTGGACCCCTGGCTTACTGCTAGCTCCACCAT 371  
 Qy 21 AlaLysTrpSerGlnAlaAlaProMetaLgLuGlyGlyGlnAsnHisGluVal 40  
 Db 372 GCCAAGTGTCCAGCTGCACCCACGACAGAA---GGAGAGCAGAAATCCCATGAAGTG 428  
 Qy 41 VallysPheMetAspValTyGlnArgSerTyrcysHisProIleGluThrLeuValAsp 60  
 Db 429 ATCAAGTTTCATGGATGCTACACGAGAGCTACTGCCGTCGATGAGACCCCTGGTGAC 488  
 Qy 61 IlePheGlnGluTyProAspGluIleGluTyrllePheLysProSerCysValProten 80  
 Db 489 ATCTTCCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCCTGTGTGCGCGTG 548  
 Qy 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 Db 549 ATGCGCTGTGAGGCTGCTGTAAACGATGAAGCCCTGGAGTGGCTGCCACGTCAGAGAGC 608  
 Qy 101 AsnIleThr 103  
 Db 609 AACATCACC 617

RESULT 7  
 BG802357 600 bp mRNA linear EST 20-DEC-2001  
 LOCUS 0174-04 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,  
 mRNA sequence.  
 DEFINITION  
 ACCESSION BG802357  
 VERSION BG802357.1 GI:17949245  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 600)  
 REFERENCE Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,  
 AUTHORS

#### TITLE

JOURNAL  
 MEDLINE  
 COMMENT  
 White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.  
 Gene expression in the developing mouse retina by EST sequencing  
 and microarray analysis  
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
 21671825  
 Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329.

#### FEATURES

Location/Qualifiers  
 1. 600  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_lib="Mouse E14.5 retina lambda ZAP II Library"  
 /tissue\_type="neural retina"  
 /dev\_stage="embryonic day 14.5 post-fertilization"  
 /note="vector: pAMP10 (Gibco); Cloned unidirectionally.  
 Primer: Oligo dt. RNA isolation: cytoplasmic RNA preps  
 (Mannatis); Cloning Technique: CUA Cloning (CloneAmp,  
 Life Technologies); Average insert size: 1.8 Kb;  
 Insertion site: TAGTCCACTGAATTCGAGTG--->. Other  
 information regarding entire library may be found at  
[http://pga.swmed.edu/Data/Libraries/microarray\\_cdna\\_librar](http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar)  
 ies.htm."

BASE COUNT 121 a 180 c 210 g 89 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4.83e-38 Length: 600  
 Score: 390.50 Matches: 72  
 Percent Similarity: 91.36% Conservative: 2  
 Best Local Similarity: 88.89% Mismatches: 6  
 Query Match: 49.31% Indels: 1  
 DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG802357 (1-600)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyLeuHisHis 20  
 Db 359 ATGAACCTTCTGCTCTCTGGTGCACTGGACCCCTGGCTTACTGCTAGCTCCACCAT 418  
 Qy 21 AlaLysTrpSerGlnAlaAlaProMetaLgLuGlyGlyGlnAsnHisGluVal 40  
 Db 419 GCCAAGTGTCCAGCTGCACCCACGACAGAA---GGAGAGCAGAAATCCCATGAAGTG 475  
 Qy 41 VallysPheMetAspValTyGlnArgSerTyrcysHisProIleGluThrLeuValAsp 60  
 Db 476 ATCAAGTTTCATGGATGCTACACGAGAGCTACTGCCGTCGATGAGACCCCTGGTGAC 535  
 Qy 61 IlePheGlnGluTyProAspGluIleGluTyrllePheLysProSerCysValProLeu 80  
 Db 536 ATCTTCCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCCTGTGTGCGCGTG 595  
 Qy 81 Met 81  
 Db 596 ATG 598

RESULT 8  
 BM991154/c 534 bp mRNA linear EST 17-JUN-2002  
 LOCUS UI-H-D10-atp-h-22-0-UI.s1 NCI\_CGAP\_D10 Homo sapiens cDNA clone  
 DEFINITION IMAGE:5862597 3', mRNA sequence.  
 ACCESSION BM991154  
 VERSION BM991154.1 GI:19710543  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 534)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Seq primer: M3 FORWARD  
 POLIA=yes.

# FEATURES

**Location/Qualifiers**  
 1. .534  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5862597"  
 /clone\_lib="NCI\_CGAP\_DI0"  
 /tissue\_type="NCI\_CGAP\_DI0"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 NCI\_CGAP\_DI0 is a cDNA library containing the following  
 tissue(s): A pool of Lung Focal Fibrosis. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 ATACCGCGTC.  
 TAG\_LIB=UI-H-DI0  
 TAG\_TISSUE=lung with fibrosis  
 TAG\_SEQ=ATACCGCGTC"

**BASE COUNT** 88 a 145 c 136 g 165 t  
**ORIGIN**

**Alignment Scores:**  
 Pred. No.: 1.95e-37 Length: 534  
 Score: 385.00 Matches: 68  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 48.61% Indels: 0  
 DB: 14 Gaps: 0

US-09-884-050-2 (1-141) x BM991154 (1-534)

QY 74 LysProSerCysValProLeuMetArgCysGlyGlyCysAsnAspGluGlu 93  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 525 AGCCCATCTGTGTCCTGATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAG 466  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 94 CysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHisGln 113  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 465 TGTGTGCCACCTGAGGAGTCCACATCACCATGCAGATTATGCGGATCAACCTCACAA 406  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 114 GlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgProLys 133  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 405 GCCCAGCACATAGGAGATGAGTCTCTTACAGCACAAACAAATGTAATGCAGACCAAG 346  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 134 LysAspArgAlaArgGlnGluLys 141  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 345 AAAGATAGACGACAGACAGAAAAA 322  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

**RESULT 9**  
 BF679862  
 LOCUS BE166230 649 bp mRNA linear EST 21-DEC-2000  
 DEFINITION 602154448F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4295651 5',  
 mRNA sequence.

**ACCESSION** BF679862  
**VERSION** BF679862.1  
**KEYWORDS** GI:11953671  
**SOURCE** EST.  
**ORGANISM** human.

Homo sapiens

**REFERENCE**  
 1 (bases 1 to 649)  
**AUTHORS** NIH-MGC http://img.nci.nih.gov/  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: CLONETECH Laboratories, Inc.  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1146 row: 0 column: 12  
 High quality sequence stop: 524.

**FEATURES**  
**source**

1. .649  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4295651"  
 /clone\_lib="NIH\_MGC\_83"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: prostate; Vector: pDMR-LIB (Clontech);  
 Site\_1: SfiI (ggccgctcgccc); Site\_2: SfiI (ggccattatggcc  
 ); 5' and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGCGGAGCGCGACATG-dT(30)BN-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA)."

**BASE COUNT** 197 a 140 c 181 g 131 t  
**ORIGIN**

**Alignment Scores:**  
 Pred. No.: 6.21e-37 Length: 649  
 Score: 382.00 Matches: 70  
 Percent Similarity: 95.95% Conservative: 1  
 Best Local Similarity: 94.59% Mismatches: 2  
 Query Match: 48.23% Indels: 1  
 DB: 12 Gaps: 0

US-09-884-050-2 (1-141) x BF679862 (1-649)

QY 47 TyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIlePheGlnGluTyrPro 66  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3 TATCAGCGCAGCTACTGCCATCAATCGAGACCTCGTGACATCTTCCAGGAGTACCCT 62  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 67 AspGluIleGluTyrIlePheLysProSerCysValProLeuMetArgCysGlyGlyCys 86  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 63 GATGAGATCGATACATCTTCAAGCCATCCTGTGTGCCCTGATGCGATGCGGGGCTGC 122  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 87 CysAsnAspGluGlyLeuGluCysValProThrGluGluSerAsnIleThrMetGlnIle 106  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 123 TGAATGACGAGGCGCTGGAGTGTGTGCCACTGAGCAGTCCCAACATCACCATGCAGATT 182  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 107 MetArgIleLysProHisGlnGln-HisIleGlyGlu 119  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 183 ATGCGGATCAAACTCAAGAGGCCAACACATTCGCGAA 222  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

**RESULT 10**  
 BE166230  
 LOCUS BE166230 208 bp mRNA linear EST 21-JUN-2000  
 DEFINITION MR3-HT0489-010300-104-g01 HT0489 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE166230

VERSION BE166230.1 GI:8628951

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 208)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR3-HT0489-010>)

300-104-g01a3-2000-03-01a4-1

Seq primer: puc 18 forward

High quality sequence stop: 208.

FEATURES

source

1..208

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0489"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

51 a 57 c 56 g 44 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 4.34e-34 Length: 208

Score: 353.00 Matches: 67

Percent Similarity: 97.10% Conservative: 0

Best Local Similarity: 97.10% Mismatches: 2

Query Match: 44.57% Indels: 1

DB: 10 Gaps: 0

US-09-884-050-2 (1-141) x BE166230 (1-208)

QY

54 ProfileGluThrLeuValAspIlePheGlnGluTyrProAspGluIleGluTyrIlePhe 73

Db

2 CCAATCGAGACCTTGTCGAC-ATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 60

QY

74 LysProSerCysValProLeuMetArgCysGlyGlyCysAsnAspGluGlyLeuGlu 93

Db

61 AAGCCATCTGTGTCCTGATGCGATGCGGGGCTGCTGCAATGACGAGGCTCGAG 120

QY

94 CysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHisGln 113

Db

121 TGTGTGCCACTGAGGAGTCCAAATCACCATGACAGATTATCGGATCAAACTCACCA 180

QY

114 GlyGlnHisIleGlyGluMetSerPhe 122

Db

181 GCCAGCACATAGGAGATGAGCTTC 207

RESULT 11

AL552344

LOCUS

DEFINITION AL552344 LTI\_NFL006\_PL2 Homo sapiens CDNA clone CS0D1069YH16 5 prime, mRNA sequence.

ACCESSION

AL552344

VERSION

AL552344.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 869)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

FEATURES

source

1..869

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="CS0D1069YH16"

/clone\_lib="LTI\_NFL006\_PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dt) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : [filang@lifetech.com](mailto:filang@lifetech.com) URL :

<http://fulllength.invitrogen.com>"

BASE COUNT 141 a 287 c 293 g 144 t

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-29 Length: 869

Score: 325.00 Matches: 55

Percent Similarity: 67.50% Conservative: 26

Best Local Similarity: 45.83% Mismatches: 35

Query Match: 41.04% Indels: 4

DB: 9 Gaps: 1

US-09-884-050-2 (1-141) x AL552344 (1-869)

QY

22 LysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41

Db

414 CAGTGGCGCTTCTCTGCT-----GGGACGGCTCTCAGAGGTGGAAGTGTA 461

QY

42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61

Db

462 CCCTTCCAGGAAGTGTGGGCGCGCAGCTACTGCCGGCGCTGAGAGGCTGTGGACGTC 521

QY

62 PheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMet 81

Db

522 GTGTCCGAGTACCCAGGAGGTGGAGCACATGTTTCAGCCCATCTGTCTCCCTGCTG 581

QY

82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSerAsn 101

Db

582 CCTCTACCGGCTGCTGGCGGATGAGATCTGCTACTGTGTSCCGGTGGAGAGGCCAAT 641

QY

102 IleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121

Db

642 GTCACCATGACAGCTCTTAAGATCCGTTCTGGGACCGCCCTCTACGTGGAGTGACG 701

QY

122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGluLys 141

Db

702 TTCTCTACGACGTTTCGCTCGAATGCGGCGCTCTGCGGAGAGAGATGAAGCGGGAAGG 761

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RESULT 12
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LOCUS          AGENCOURT_8540206 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297259
DEFINITION    5', mRNA sequence.
ACCESSION     BQ644755
VERSION       BQ644755.1 GI:21768927
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 890)
AUTHORS       NIH-MGC http://mgi.cni.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: CGAP (Stanford)
               cDNA Library Preparation: Rubin Laboratory
               DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
               Clone distribution: MGC Clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM2506 row: g column: 20
               High quality sequence stop: 662.
FEATURES      source
               1..890
               Location/Qualifiers
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                 /db_xref="taxon:9606"
                 /clone="IMAGE:6297259"
                 /clone_lib="NIH_MGC_100"
                 /tissue_type="hepatocellular carcinoma, cell line"
                 /lab_host="DH10B (phage-resistant)"
                 /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                 into EcoRI/XhoI sites using the following 5' adaptor:
                 GGCAGCAG(G). Size-selected >500bp for average insert size
                 1.8kb. Library constructed by Ling Hong in the laboratory
                 of Gerald M. Rubin (University of California, Berkeley)
                 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                 II RT (Life Technologies). Note: this is a NIH_MGC
                 Library."
BASE COUNT    183 a 259 c 265 g 182 t 1 others
ORIGIN
Alignment Scores:
Pred. No.:    1.23e-29      Length:      890
Score:        325.00      Matches:      55
Percent Similarity: 67.50%      Conservative: 26
Best Local Similarity: 45.83%      Mismatches:   35
Query Match:  41.04%      Indels:       4
DB:           14          Gaps:         1

US-09-884-050-2 (1-141) x BQ644755 (1-890)

QY  22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41
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QY  42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
Db  338 CCCTCCAGAGAGTGTGGGGCGGCAGCTACTCGGGCGCTCGAGAGGTGTGTGACGTC 397
QY  62 PheGlnGluTyrProAspGluLeuGlyTyrIlePheLysProSerCysValProLeuMet 81
Db  398 GTGTCCGAGTACCCAGCGAGGTGGAGCACATGTTTCAGCCCATCTGTCTCTCCCTGTG 457
QY  82 ArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsn 101
Db  458 CGCTGCACCGCGCTGTGGCGCGCATGAGAAATCTGCATCTGTCTGCGGTGGAGACGCCCAAT 517

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QY  102 IleThrMetGlnIleMetArgTyleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121
Db  518 GTCACCATGCAGCTCTTAAGATCGTCTGGGGACCGCCCTCTACCTGAGCTGAGCG 577
QY  122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGluLys 141
Db  578 TTCTCTCAGCAGCTTCGCTGCGAATGCGCGCTCTGCGGGAGAAGATGAAGCGGAAGG 637

RESULT 13
AL552106      901 bp      mRNA      linear      EST 16-FEB-2001
LOCUS          AL552106 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI059N23 5
DEFINITION    prime, mRNA sequence.
ACCESSION     AL552106
VERSION       AL552106.1 GI:12890686
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 901)
AUTHORS       Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES      source
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                 /tissue_type="placenta"
                 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                 was primed with a NotI-oligo(dT) primer. Five prime end
                 enriched, double-stranded cDNA was digested with Not I and
                 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                 vector. Library was normalized. Library was constructed by
                 Life Technologies. Contact : Feng Liang Life Technologies,
                 a division of Invitrogen 9800 Medical Center Drive
                 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                 Email : fliang@lifetech.com URL :
                 http://fulllength.invitrogen.com"
BASE COUNT    148 a 298 c 299 g 153 t 3 others
ORIGIN
Alignment Scores:
Pred. No.:    1.25e-29      Length:      901
Score:        325.00      Matches:      55
Percent Similarity: 67.50%      Conservative: 26
Best Local Similarity: 45.83%      Mismatches:   35
Query Match:  41.04%      Indels:       4
DB:           9          Gaps:         1

US-09-884-050-2 (1-141) x AL552106 (1-901)

QY  22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41
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QY  42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
Db  455 CCCTTCAGAGAGTGTGGGGCGGCAGCTACTCGGGCGCTGGAGAGGTGTGTGACGTC 514
QY  62 PheGlnGluTyrProAspGluLeuGlyTyrIlePheLysProSerCysValProLeuMet 81
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QY  82 ArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsn 101
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Db 575 CGTGCACCGGCTGCTGGCGGATGAGAAATCTGCACCTGTGTGCGGTGGAGACGCCCAAT 634
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Qy 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaAArgGlnGluLys 141
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Db 695 TTCTCTCAGCAGCTGTGCTGGAATGCGGCTCTGCGGAGAGATGAAGCCGGAAGG 754

RESULT 14
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LOCUS
DEFINITION AL546005 LTI_NFL006_PL2 903 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL546005
VERSION AL546005.1 GI:12878718
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 148 a 296 c 294 g 157 t 8 others
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-29 Length: 903
Score: 325.00 Matches: 55
Percent Similarity: 67.50% Conservative: 26
Best Local Similarity: 45.83% Mismatches: 35
Query Match: 41.04% Indels: 4
DB: 9 Gaps: 1
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Qy 22 LysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluValVal 41
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Db 508 GTGTCCGAGTACCCAGGAGGTGGAGCAATGTTACCCCATCTCTGTCTCCCTGCTG 567
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Qy 82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsn 101

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Db 568 CGTGCACCGGCTGCTGGCGGATGAGAAATCTGCACCTGTGTGCGGTGGAGACGCCCAAT 627
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Db 628 GTACCATGACGAGCTCTAAAGATCGTCTGTGGGACCGCCCTCTAGCTGAGCTGAGC 687
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LOCUS
DEFINITION AL547463 LTI_NFL006_PL2 925 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL547463
VERSION AL547463.1 GI:12881556
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 148 a 309 c 301 g 161 t 6 others
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-29 Length: 925
Score: 325.00 Matches: 55
Percent Similarity: 67.50% Conservative: 26
Best Local Similarity: 45.83% Mismatches: 35
Query Match: 41.04% Indels: 4
DB: 9 Gaps: 1
US-09-884-050-2 (1-141) x AL547463 (1-925)
Qy 22 LysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluValVal 41
   ::::::::::::::::::::
Db 404 CAGTGGGCTTGTCTGCT-----GGGAACGCTCTGTCTGAGAGGTGAAGTGTA 451
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Qy 42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
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Db 452 CCCTTCCAGGAAGTGTGGGCGGAGCTACTGCGGGCGCTGGAGAGGCTGTGTGACGTC 511
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Qy 62 PheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMet 81
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Db 512 GTGTCCGAGTACCCAGGAGGTGGAGCAATGTTACCCCATCTCTGTCTCCCTGCTG 571
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QY 82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSerAsn 101  
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QY 102 IleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121  
Db 632 GTACCATGCAGCTCCTAAAGATCCGTTCTGGGGACCGGCCCTCTACGTGGAGCTGACG 691  
QY 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGluLys 141  
Db 692 TTCTCTCAGCAGCTTCGCTGCCAATGCCGCCCTCTCGGGGAGAAGATGAAGCCGGAAGG 751

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Job time : 2163 secs